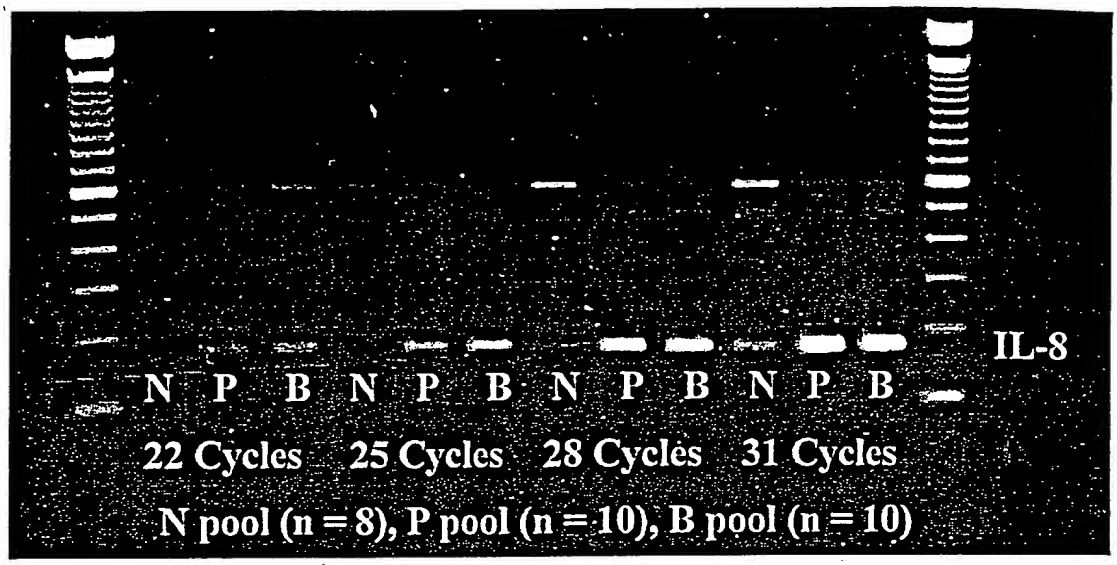

IL-8
N P B N P B N P B N P B
22 Cycles 25 Cycles 28 Cycles 31 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 1A

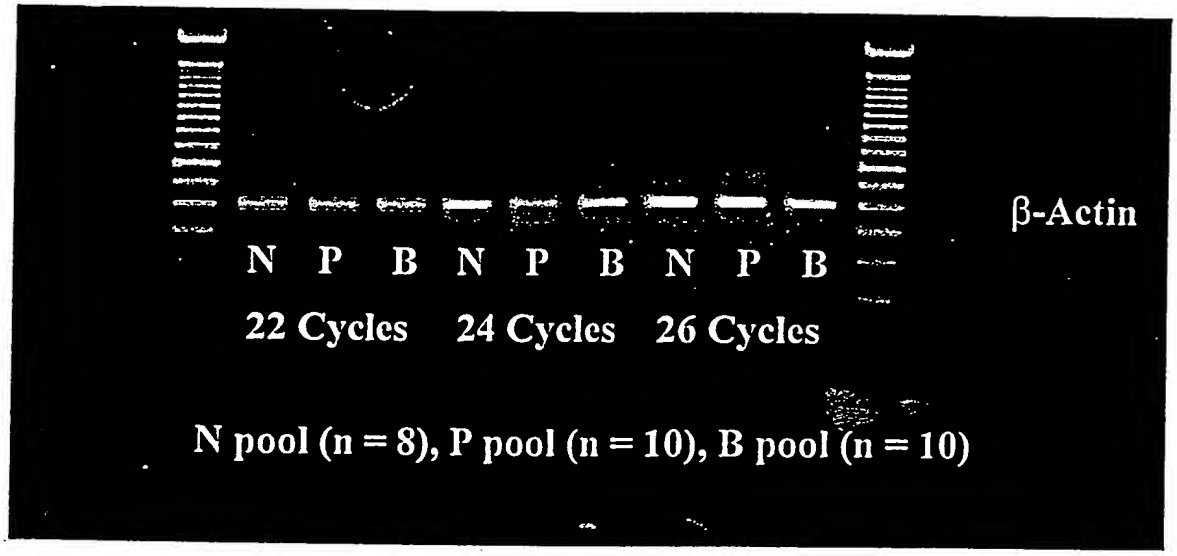

β-Actin
N P B N P B N P B
22 Cycles 24 Cycles 26 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 1B

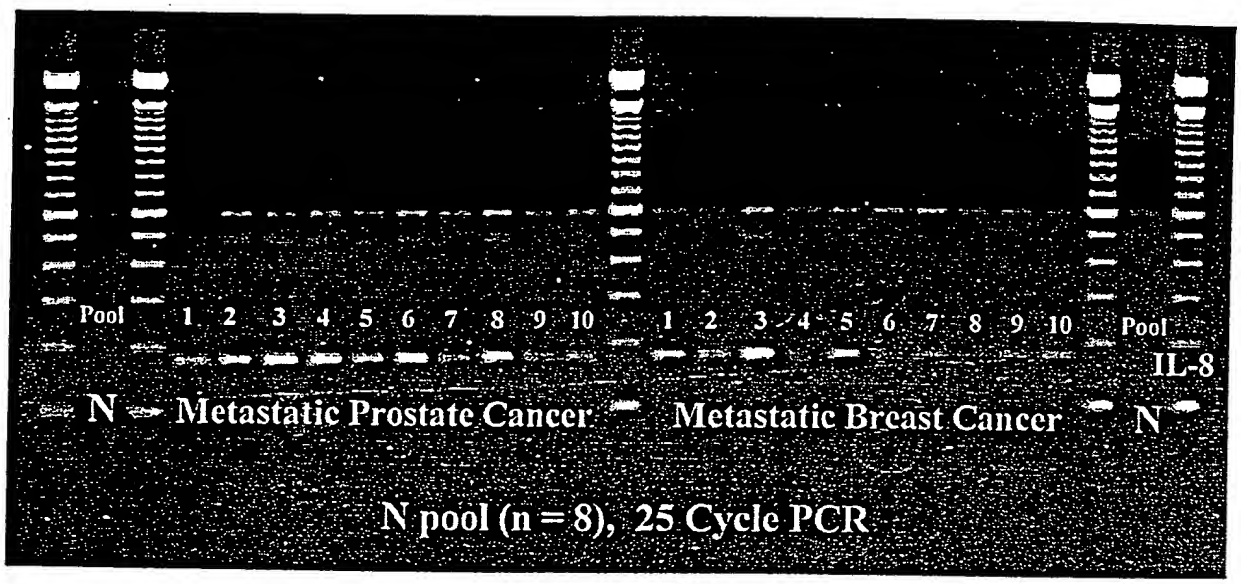

Pool
1 2 3 4 5 6 7 8 9 10
1 2 3 4 5 6 7 8 9 10
Pool
IL-8
N
Metastatic Prostate Cancer
Metastatic Breast Cancer
N
N pool (n = 8), 25 Cycle PCR

FIG. 2A

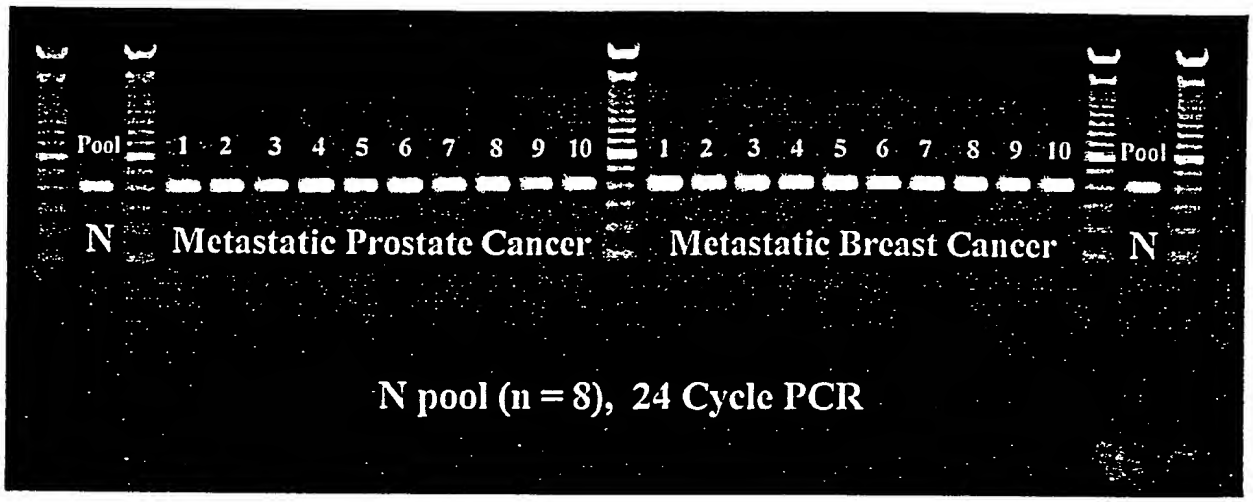

Pool
1 2 3 4 5 6 7 8 9 10
1 2 3 4 5 6 7 8 9 10
Pool
N
Metastatic Prostate Cancer
Metastatic Breast Cancer
N
N pool (n = 8), 24 Cycle PCR

FIG. 2B

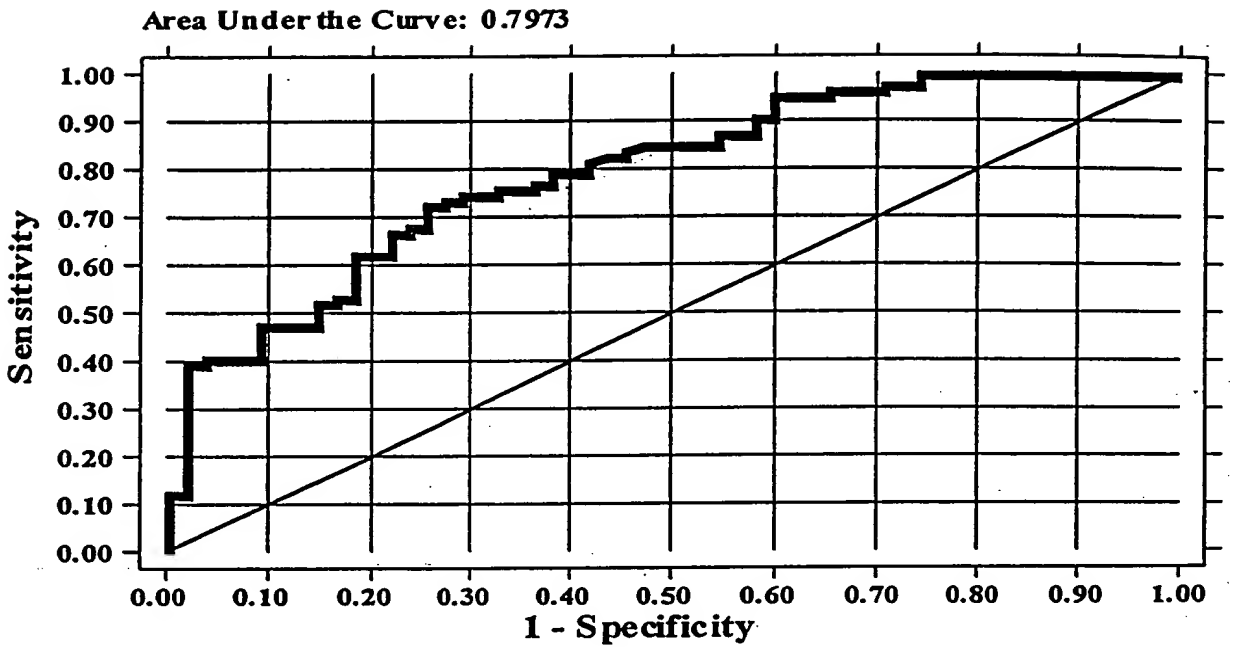

Area Under the Curve: 0.7973
Sensitivity
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0.00
0.10
0.20
0.30
0.40
0.50
0.60
0.70
0.80
0.90
1.00
1 - Specificity

FIG. 3

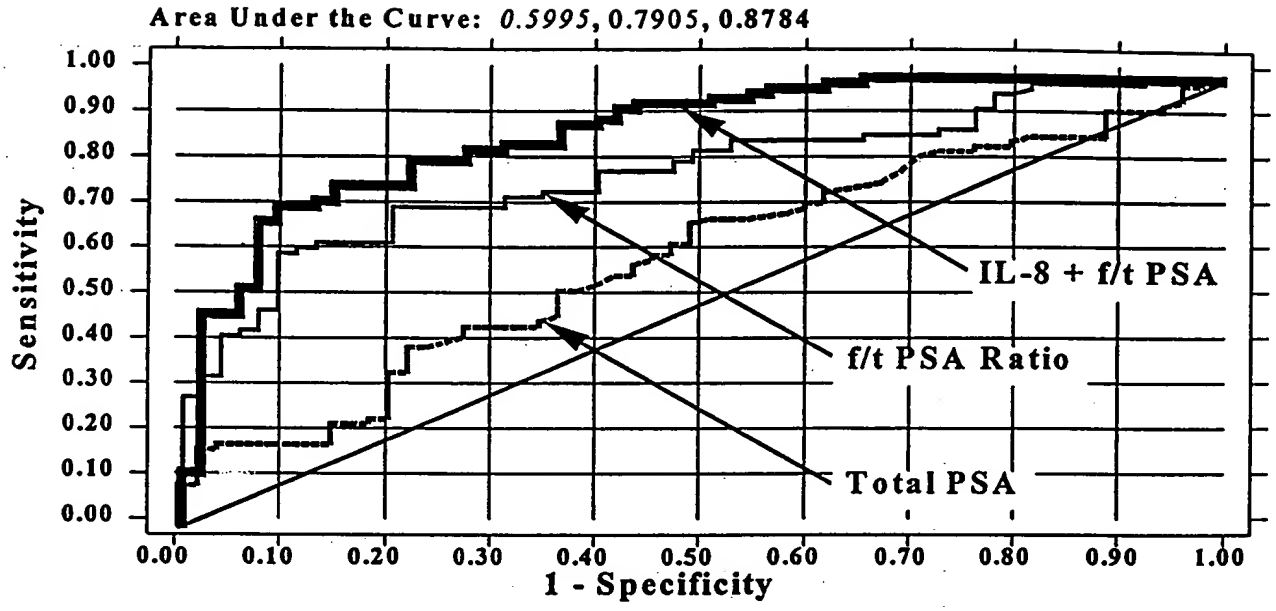

Area Under the Curve: 0.5995, 0.7905, 0.8784
Sensitivity
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0.00
0.10
0.20
0.30
0.40
0.50
0.60
0.70
0.80
0.90
1.00
1 - Specificity
IL-8 + f/t PSA
f/t PSA Ratio
Total PSA

FIG. 4

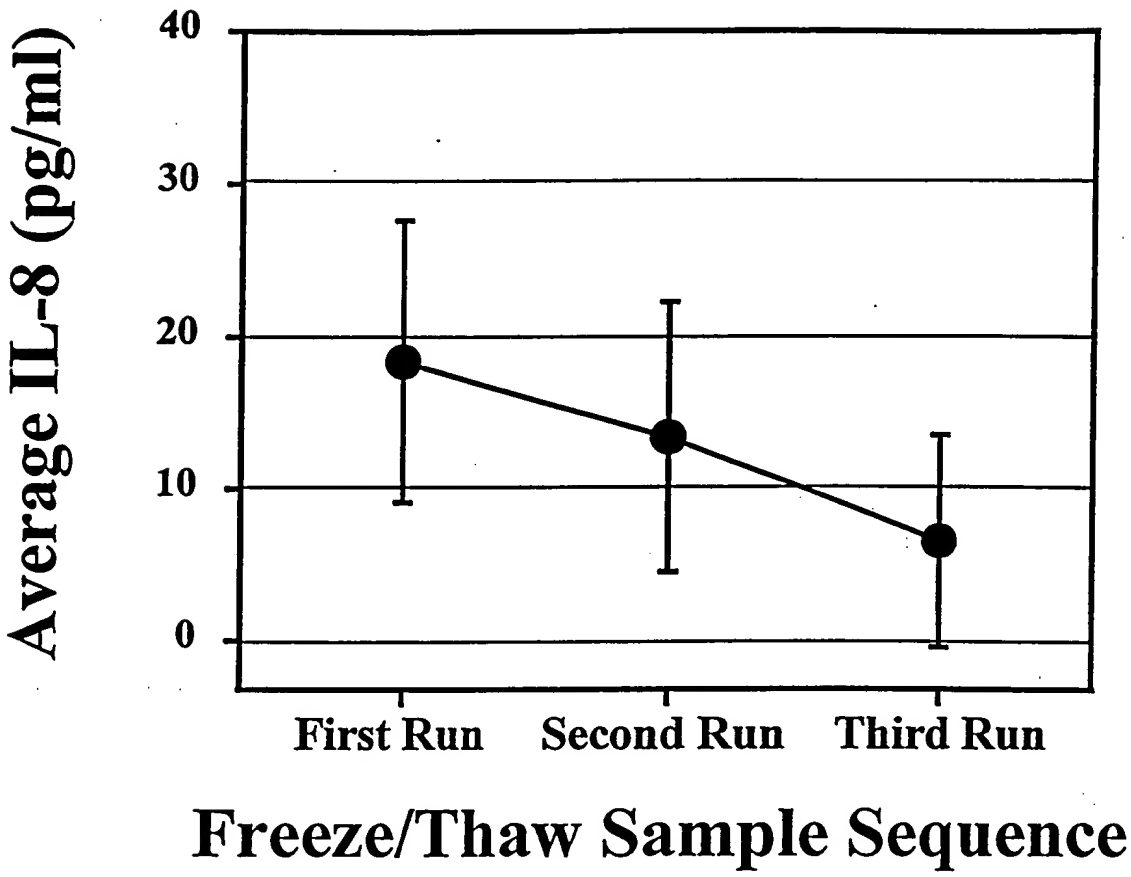

Average IL-8 (pg/ml)
40
30
20
10
0
First Run
Second Run
Third Run
Freeze/Thaw Sample Sequence

FIG. 5

```
                                30                                  60
GCGGCAGGCGCGGCAAATTACGTTGCCGGAGCTGAACGGCGCGGCTGGTCTGAAGGCAAA HUM-UC331

                                90                                 120
CAAGCGAGCGAGCGCGCGATAGGGGCCGAGAGGACGCGCAGGTGGCGGCGTTGCCATGTC HUM-UC331
                                                        START
                               150                                 180
GCACGGTCACAGCCACGGCGGGGGTGGCTGCCGCTGCGCCGCCGAACGGGAGGAGCCGCC HUM-UC331

                               210                                 240
CGAGCAGCGCGGCCTGGCCTACGGCCTGTACCTGCGCATCGACCTGGAGCGGCTGCAATG HUM-UC331

                               270                                 300
CCTTAACGAGAGCCGCGAGGGCAGCGGCCGCGGCGTCTTCAAGCCATGGGAGGAGCGGAC HUM-UC331
                                        TTTCAAGCCGTGGGAGGA-CGGAC MOU-UC331
                                        *                   *
                               330                                 360
CGACCGCTCCAAGTTTATTGAAAGTGATGCAGATGAAGAGCTTCTGTTTAATATTCCATT HUM-UC331
CGACCGCTCCAAGTTCGCTGAAAGTGATGCGGACGAAGAGCTCCTGTTTAATATTCCGTT MOU-UC331
              * *               *   *         *                 *
                               390                                 420
TACGGGCAATGTCAAGCTCAAAGGCATCATTATAATGGGAGAGGATGATGACTCACACCC HUM-UC331
TACGTGCAATGTCAAGCTGAAAGGCGTCATCATAATGGGCGAGGATGATGACTCGCACCC MOU-UC331
    *               *     *     *         *                 *
```

FIG. 6A

```
                                450                                 480
CTCTGAGATGAGACTGTACAAGAATATTCCACAGATGTCCTTTGATGATACAGAAAGGGA HUM-UC331
CTCGGAGATGAGACTGTACAAGAACATTCCACAGATGTCATTTGATGACACAGAAAGGGA MOU-UC331
   *                    *                   *       *

                                510                                 540
GCCAGATCAGACCTTTAGTCTGAACCGGGATCTTACAGGAGAATTAGAGTATGCTACAAA HUM-UC331
GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAATTAGAATATGCTACGAA MOU-UC331
                 *           *  **                 *         *

                                570                                 600
AATTTCTCGTTTTTCAAATGTCTATCATCTCTCAATTCATATTTCAAAAAACTTCGGAGC HUM-UC331
AATCTCCAGGTTTTCAAATGTCTATCATCTTTCCATTCATATTTCAAAAAACTTTGGAGC MOU-UC331
   *  *  *                    ** *  *                      *

                                630                                 660
AGATACGACAAAGGTCTTTTATATTGGCCTGAGAGGAGAGTGGACTGAGCTTCGCCGACA HUM-UC331
AGATACGACGAAGATCTTTTATATTGGCCTGCGGGGAGAGTGGACTGAGCTTCGCCGGCA MOU-UC331
         *   *                   * *                          *

                                690                                 720
CGAGGTGACCATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATAGGGTCCATCA HUM-UC331
TGAGGTGACCATCTGCAACTATGAAGCGTCAGCCAACCCAGCAGACCACCGGGTGCATCA MOU-UC331
*                   *  *     *  *                    **     *

                                750                                 780
GGTTACCCCACAGACACACTTTATTTCCTAAGGGCTGGCCAAGGCTCCCATAGAGGCGCT HUM-UC331
GGTCACCCCGCAGACACACTTCATTTCTTAAGGGCCAGCCGGGGCTCCCTCAGATGCGCT MOU-UC331
   *     *             *     *STOP   **   **        **   *
```

FIG. 6B

```
                                 810                                 840
GTGTCAGTGAAGATGTACGACTACCTGTTGGGAAGGACAAAGGGATGAGGCTCCAGAGAG HUM-UC331
GTTAGTGAA--GATGTGCGACCACCTGCTGGGAAGGACAGAGG-ATG---CTCCAGCAAT MOU-UC331
  **** ****      *    *     *           *   *   ***       ** *

                                 870                                 900
AGTTGGCTGCCACAGCTCTG-CCAAGCTTTGTCTTTGGGGCTTGCTGCAGAAACCTGGCC HUM-UC331
AGTTGCCTGCCAGAGCTTTGGCCAGGCTTTGTC-TCGGGG-TTGCTGCAGGAACCTGGCC MOU-UC331
     *       *    * *   *         * *    *          *

                                 930                                 960
TACGGAAGATACGACACCACTGGGAGGGTTGTGTAGGTGCCAGGGGACCATCGTGGTTCT HUM-UC331
TGTGGAAACCGCCTCACCACCAGGAGCG--GTATGGGTGCCAAGGGA---TAGTCTCTCT MOU-UC331
 **    **** **       **    * **  * *        *    *** *  ***

                                 990                                1020
CTAGGGCGCTGTGGAAATTGGGTCTTGGGCTGGGTGGCATCTGGCAGTCATGGGTAACAC HUM-UC331
CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAGTCATGAATAATGC MOU-UC331
   *   *   **    *         *                  *         **   **

                                1050                                1080
TTGCTTTTCCAGTTAATGTGGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT HUM-UC331
TCACTT-CCCAGTC--TGTGGCCACGGGATCCCATGTGTCTTTTTGCTT-GATTTCTTGT MOU-UC331
 **   **      ***          * *   *   *     * *       *  *******

                                1110                                1140
GTTGTGTGACTTGTTTTTTTGATTTTGTATTTGTTTTTTTAAAGGAAACTATTTGTGGGC HUM-UC331
GTGGTTTGTCCT-TTTGTGGCA-------------TCAAAAAGGATGCTTCCTTGACCG MOU-UC331
  *   *   *    *   * *** ************** ***       **   *** ******
```

FIG. 6C

DOCUMENT BASED

```
                                1170                                1200
TATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTAGCCATCAGGAGGGTCTCC HUM-UC331
TAGAAT---CCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGGTCTCC MOU-UC331
  * ***** *       **  **** *  *      *  **

                                1230                                1260
AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTCCCCTCTCATTGTTCAGCATTCTTGTC HUM-UC331
AGCTAGAAACACTTCGTCCCTGCTTGCTCCT-CCTCCTGTCATTGCTCAGCATTCGTGTC MOU-UC331
 *   *         *  *                ** *   *      *          *

                                1290                                1320
AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGG HUM-UC331
AGGGTGCCTAGCT-GGTGTCACATATCAGACACAAGTGTCCCACAATGGTGGTTGGAAAG MOU-UC331
 * *    *    *  *  **** *   **    *     ***** ** * * *   *

                                1350                                1380
ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGC HUM-UC331
GAAGGAGTCTCCTG---ATACATGACTGCTT------GGGG--AAGG-CTTACACAGT-C MOU-UC331
**              ***  * *   **    ******    **    *   ***  * *

                                1410                                1440
CTAGCTAAGCAGTCTGGGGAGAGCATGGGGATCATTTCTATGTGTGTGGGTAATCTGGTC HUM-UC331
TAGCCAAATTAGTT--GCGAG----------TCCTTTCCCTGTGT--GGGTGACCTGGTT MOU-UC331
**** *  **   *** *   **********  *    **     **    * *     *

                                1470                                1500
AG--TAAGATTGAGACTTAGTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT HUM-UC331
GGGGTAAAACTGAGACAG--TAAAGATTCCTCTTGGGACCTCCTTGGTGTTTCCCTGCTT MOU-UC331
* **   * *       **** *         *     * **     **     ****
```

FIG. 6D

```
                                1530                                1560
CTAACTAGTGTTGTAAGTCCGATGCCAGAATTTGGAGATTTGAGTTCTTCTTTTCATGGC HUM-UC331
CTAACTCATGTTATAAACCCAGGGCTGGAGTCTGGAGACCCTGCTCCTTCTGTTCATGGC MOU-UC331
      **    *   **  ***  **  * *      ****** *     *

                                1590                                1620
TTTTATTCACTGTGACTAATAAGCTTCCTAATAAATCCTTGCCAGACTTAAAAAAAAAAA HUM-UC331
TTTCATTCATGGTGACTAATGAGCTTCCTAATAAATCCTTAG-AGACTTAAAA         MOU-UC331
   *     **          *                     * *
```

FIG. 6E

```
         10         20         30         40
 MSHGHSHGGGGCRCAAER-EEPPEQRGLAYGLYLRIDLE HUM-UC331
>CSHGHSHN-----CAAEHIPEVPGDDVYRYDMVSYIDME ZK353.1

         50         60         70         80
RLQCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF HUM-UC331
                  >FKPWEERTDRSKFAESDADEELLF MOU-UC331
KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF ZK353.1


         90        100        110        120
NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPQMSFDD HUM-UC331
NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPQMSFDD MOU-UC331
NIPFTGHVRLTGLSIIGDEDGSHPAKIRLFKDREAMSFDD ZK353.1

        130        140        150        160
TEREPDQTFSLNRDLTGELEYATKISRFSNVYHLSIHISK HUM-UC331
TEREPEQTFSLNRDITGELEYATKISRFSNVYHLSIHISK MOU-UC331
CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA ZK353.1

        170        180        190        200
NFGADTTKVFYIGLRGEWTELRRHEVTICNYEASANPADH HUM-UC331
NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH MOU-UC331
NFGEDETKIYYIGLRGEFQHEFRQRIAIATYESRAQLKDH ZK353.1

        210
RVHQVTPQTHFIS. HUM-UC331
RVHQVTPQTHFIS. MOU-UC331
KNEIPDAVAKGLF. ZK353.1
```

FIG. 7

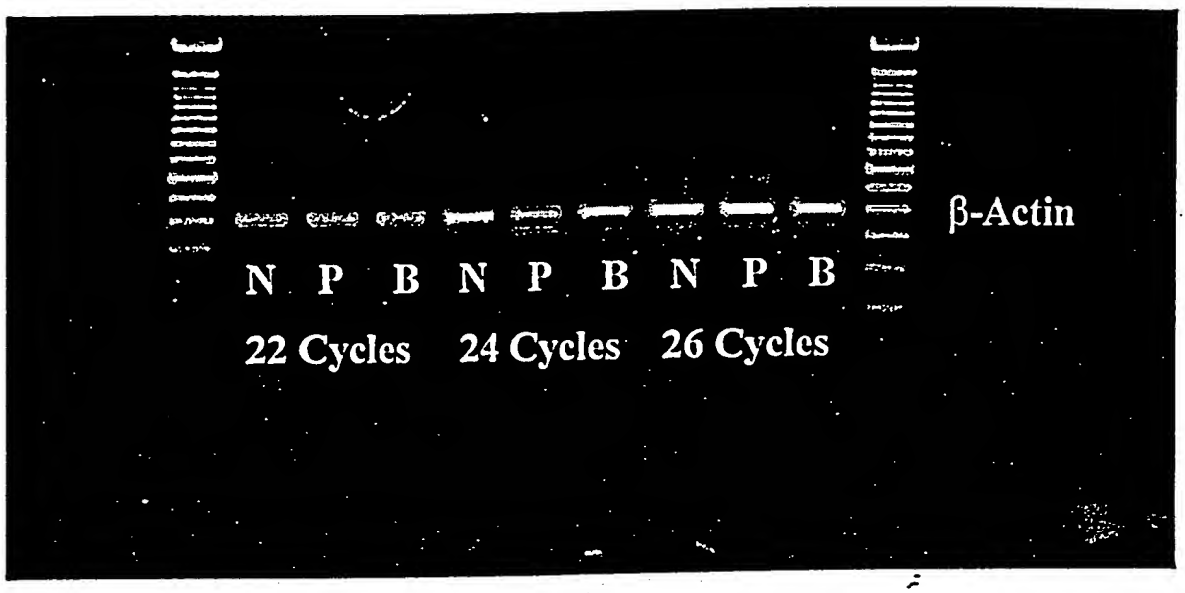
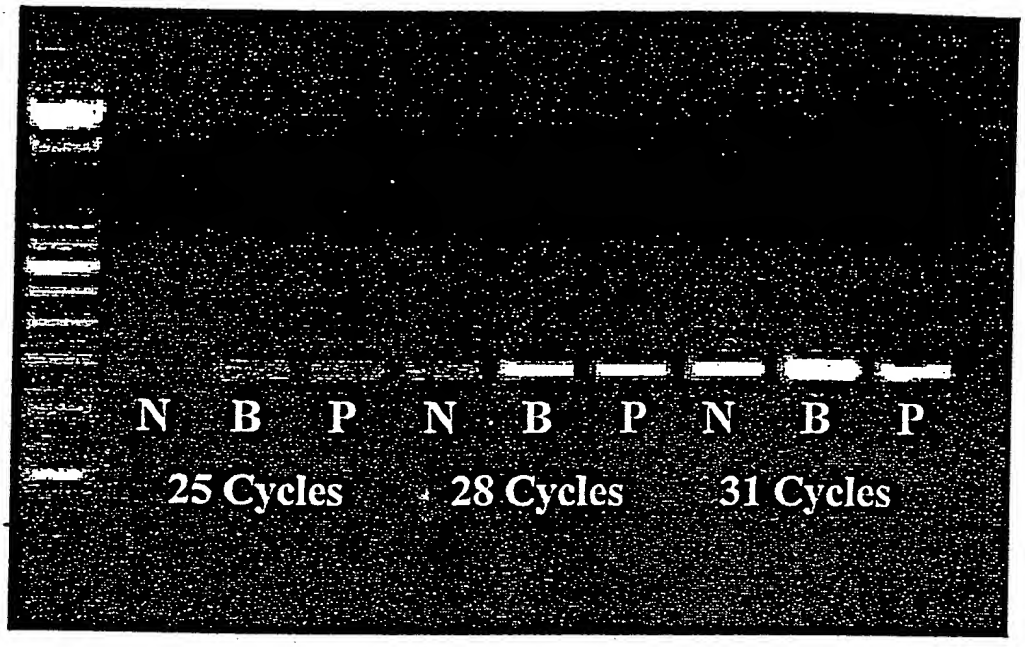


FIG. 8A



UC331

FIG. 8B

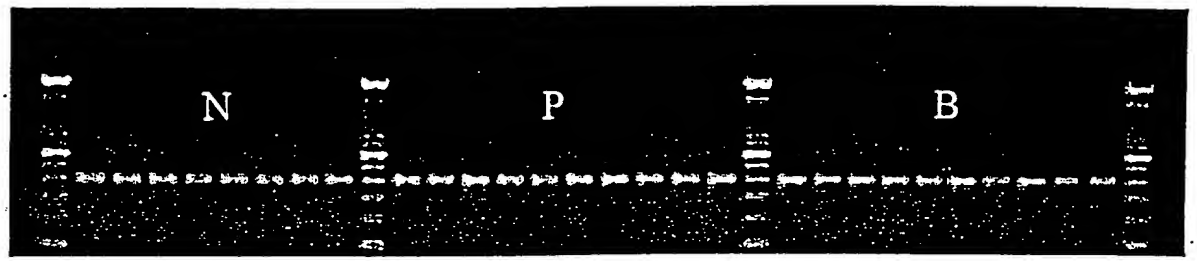


FIG. 9A

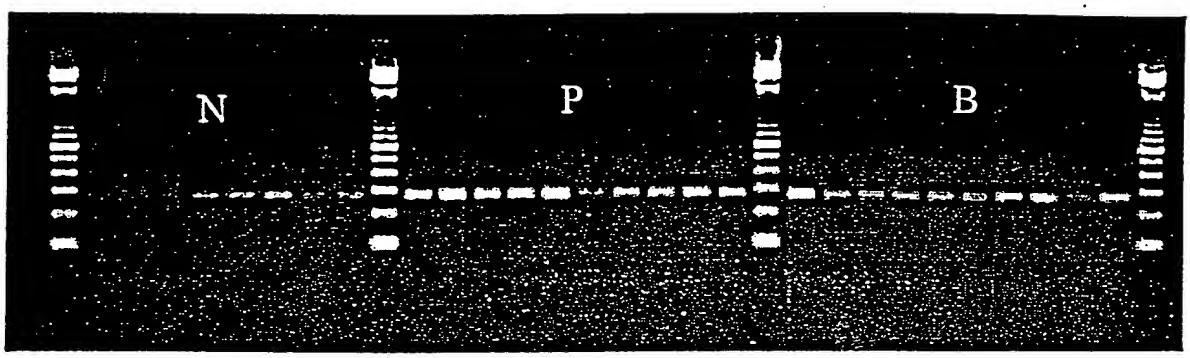


FIG. 9B

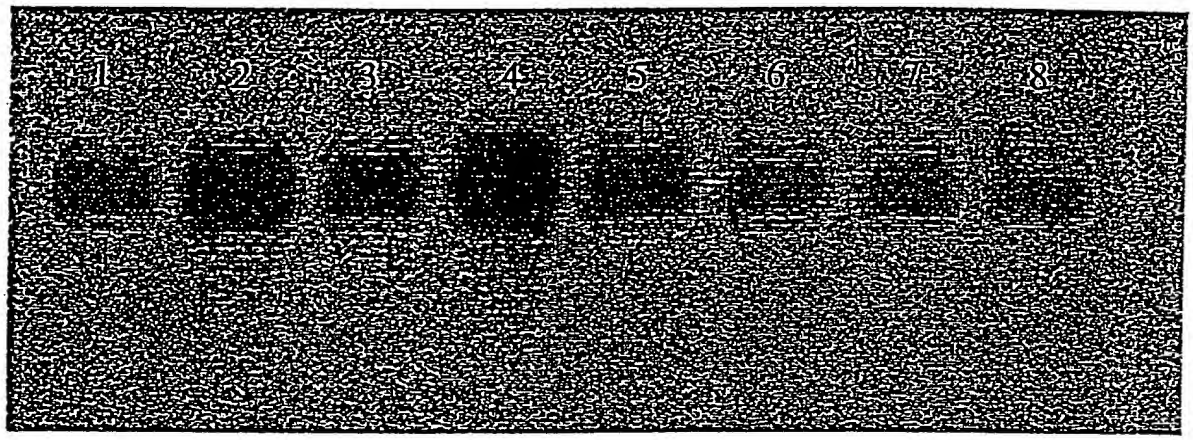


FIG. 10

```
        10          20          30          40          50
CGACTCGTCG CCATTCCCGG AGCAGGTCGG CCTCGGCCCA GGGGCGAGTA
        60          70          80          90         100
TCCGTTGCTG TGTCGGAGAC ACTAGTCCCC GACACCGAGA CAGCCAGCCC
       110         120         130         140         150
TCTCCCCTGC CTCGCGGCGG GAGAGCGTGT CCGGCCGGCC GGCCGGCGGG
       160         170         180         190         200
GCTCGCGCAA CCTCCCTCGC CTCCCCTTCC CCCGCAGCCT CCGCCCCGCC
       210         220         230         240         250
AGGCCCGGCC CGGACTCCCG AGCCCCGGCC TCCTCGTCCT CGGTCGCCGC
       260         270         280         290         300
TGCCGCCGGG CTTAACAGCC CCGTCCGCCG CTTCTCTTCC TAGTTTGAGA
       310         320         330         340         350
AGCCAAGGAA GGAAACAGGG AAAAATGTCG CCATGAAGGC CGAGAACCGC
       360         370         380         390         400
TGCCGCCGCC GACCCCCGCC GGCCCTGAAC GCCATGAGCC TGGGTCCCCG
       410         420         430         440         450
CCGCGCCCGC TCCGCTCCGA CTGCCGTCGC CGCCGAGGCC CCCGTTGATG
       460         470         480         490         500
CCGCTGAGCT CCCCCAACGC CGCCGCCACC GCCTCCGACA TGGACAAGAA
       510         520         530         540         550
CAGCGGCTCC AACAGCTCCT CCGCCTCTTC GGGCAGCAGC AAAGGGCAAC
       560         570         580         590         600
AGCCGCCCCG CTCCGCCTCG GCGGGGCCAG CCGGCGAGTC TAAACCCAAG
       610         620         630         640         650
AGCGAATTAC TAATTTCAGC TGGATTCAAT TTGTTGTCAG TTGATTCTGT
       660         670         680         690       698
AGTAAGGCCA TATGTTGCCC CTCTGGAGGT GCTTGTCAAC TACTCTGG

ATG ATG GAT GGA AAG AAC TCC AGT GGA TCC AAG CGT TAT AAT 740
Met Met Asp Gly Lys Asn Ser Ser Gly Ser Lys Arg Tyr Asn 14

CGC AAA CGT GAA CTT TCC TAC CCC AAA AAT GAA AGT TTT AAC 782
Arg Lys Arg Glu Leu Ser Tyr Pro Lys Asn Glu Ser Phe Asn 28

AAC CAG TCC CGT CGC TCC AGT TCA CAG AAA AGC AAG ACT TTT 824
Asn Gln Ser Arg Arg Ser Ser Ser Gln Lys Ser Lys Thr Phe 42

AAC AAG ATG CCT CCT CAA AGG GGC GGC GGC AGC AGC AAA CTC 866
Asn Lys Met Pro Pro Gln Arg Gly Gly Gly Ser Ser Lys Leu 56

TTT AGC TCT TCT TTT AAT GGT GGA AGA CGA GAT GAG GTA GCA 908
Phe Ser Ser Ser Phe Asn Gly Gly Arg Arg Asp Glu Val Ala 70

GAG GCT CAA CGG GCA GAG TTT AGC CCT GCC CAG TTC TCT GGT 950
Glu Ala Gln Arg Ala Glu Phe Ser Pro Ala Gln Phe Ser Gly 84

CCT AAG AAG ATC AAC CTG AAC CAC TTG TTG AAT TTC ACT TTT 992
Pro Lys Lys Ile Asn Leu Asn His Leu Leu Asn Phe Thr Phe 98

GAA CCC CGT GGC CAG ACG GGT CAC TTT GAA GGC AGT GGA CAT 1034
Glu Pro Arg Gly Gln Thr Gly His Phe Glu Gly Ser Gly His 112
```

FIG. 11A

GGT AGC TGG GGA [redacted]G AGG AAC AAG TGG GGA CAT A[redacted]CCT TTT 1076
Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe 126

AAC AAG GAA CTC TTT TTA CAG GCC AAC TGC CAA TTT GTG GTG 1118
Asn Lys Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val 140

TCT GAA GAC CAA GAC TAC ACA GCT CAT TTT GCT GAT CCT GAT 1160
Ser Glu Asp Gln Asp Tyr Thr Ala His Phe Ala Asp Pro Asp 154

ACA TTA GTT AAC TGG GAC TTT GTG GAA CAA GTG CGC ATT TGT 1202
Thr Leu Val Asn Trp Asp Phe Val Glu Gln Val Arg Ile Cys 168

AGC CAT GAA GTG CCA TCT TGC CCA ATA TGC CTC TAT CCA CCT 1244
Ser His Glu Val Pro Ser Cys Pro Ile Cys Leu Tyr Pro Pro 182

ACT GCA GCC AAG ATA ACC CGT TGT GGA CAC ATC TTC TGC TGG 1286
Thr Ala Ala Lys Ile Thr Arg Cys Gly His Ile Phe Cys Trp 196

GCA TGC ATC CTG CAC TAT CTT TCA CTG AGT GAG AAG ACG TGG 1328
Ala Cys Ile Leu His Tyr Leu Ser Leu Ser Glu Lys Thr Trp 210

AGT AAA TGT CCC ATC TGT TAC AGT TCT GTG CAT AAG AAG GAT 1370
Ser Lys Cys Pro Ile Cys Tyr Ser Ser Val His Lys Lys Asp 224

CTC AAG AGT GTT GTT GCC ACA GAG TCA CAT CAG TAT GTT GTT 1412
Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val 238

GGT GAT ACC ATT ACG ATG CAG CTG ATG AAG AGG GAG AAA GGG 1454
Gly Asp Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly 252

GTG TTG GTG GCT TTG CCC AAA TCC AAA TGG ATG AAT GTA GAC 1496
Val Leu Val Ala Leu Pro Lys Ser Lys Trp Met Asn Val Asp 266

CAT CCC ATT CAT CTA GGA GAT GAA CAG CAC AGC CAG TAC TCC 1538
His Pro Ile His Leu Gly Asp Glu Gln His Ser Gln Tyr Ser 280

AAG TTG CTG CTG GCC TCT AAG GAG CAG GTG CTG CAC CGG GTA 1580
Lys Leu Leu Leu Ala Ser Lys Glu Gln Val Leu His Arg Val 294

GTT CTG GAG GAG AAA GTA GCA CTA GAG CAG CAG CTG GCA GAG 1622
Val Leu Glu Glu Lys Val Ala Leu Glu Gln Gln Leu Ala Glu 308

GAG AAG CAC ACT CCC GAG TCC TGC TTT ATT GAG GCA GCT ATC 1664
Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala Ala Ile 322

CAG GAG CTC AAG ACT CGG GAA GAG GCT CTG TCG GGA TTG GCC 1706
Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala 336

GGA AGC AGA AGG GAG GTC ACT GGT GTT GTG GCT GCT CTG GAA 1748
Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu 350

FIG. 11B

CAA CTG GTG CT[redacted]TG GCT CCC TTG GCG AAG GAG [redacted]GTT TTT 1790
Gln Leu Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe 364

CAA CCC AGG AAG GGT GTG CTG GAG TAT CTG TCT GCC TTC GAT 1832
Gln Pro Arg Lys Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp 378

GAA GAA ACC ACG GAA GTT TGT TCT CTG GAC ACT CCT TCT AGA 1874
Glu Glu Thr Thr Glu Val Cys Ser Leu Asp Thr Pro Ser Arg 392

CCT CTT GCT CTC CCT CTG GTA GAA GAG GAG GAA GCA GTG TCT 1916
Pro Leu Ala Leu Pro Leu Val Glu Glu Glu Glu Ala Val Ser 406

GAA CCA GAG CCT GAG GGG TTG CCA GAG GCC TGT GAT GAC TTG 1958
Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala Cys Asp Asp Leu 420

GAG TTA GCA GAT GAC AAT CTT AAA GAG GGG ACC ATT TGC ACT 2000
Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile Cys Thr 434

GAG TCC AGC CAG CAG GAA CCC ATC ACC AAG TCA GGC TTC ACA 2042
Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr 448

CGC CTC AGC AGC TCT CCT TGT TAC TAC TTT TAC CAA GCG GAA 2084
Arg Leu Ser Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu 462

GAT GGA CAG CAT ATG TTC CTG CAC CCT GTG AAT GTG CGC TGC 2126
Asp Gly Gln His Met Phe Leu His Pro Val Asn Val Arg Cys 476

CTC GTG CGG GAG TAC GGC AGC CTG GAG AGG AGC CCC GAG AAG 2168
Leu Val Arg Glu Tyr Gly Ser Leu Glu Arg Ser Pro Glu Lys 490

ATC TCA GCA ACT GTG GTG GAG ATT GCT GGC TAC TCC ATG TCT 2210
Ile Ser Ala Thr Val Val Glu Ile Ala Gly Tyr Ser Met Ser 504

GAG GAT GTT CGA CAG CGT CAC AGA TAT CTC TCT CAC TTG CCA 2252
Glu Asp Val Arg Gln Arg His Arg Tyr Leu Ser His Leu Pro 518

CTC ACC TGT GAG TTC AGC ATC TGT GAA CTG GCT TTG CAA CCT 2294
Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu Ala Leu Gln Pro 532

CCT GTG GTC TCT AAG GAA ACC CTA GAG ATG TTC TCA GAT GAC 2336
Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser Asp Asp 546

ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378
Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560

GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420
Glu Arg Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574

AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462
Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

FIG. 11C

```
CTA CAG CAG TTT CCC GCC TTC AAT TCT TAT ACC TGC TCC TCT 2504
Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602

GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546
Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616

CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588
Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630

GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630
Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644

AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672
Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658

TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714
Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672

GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756
Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686

AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798
Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700

GAT AAT TCA GAC CGT GTT CCT GTG CCC AGT TTT CAA AAT TCC 2840
Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714

TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882
Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728

CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA GGA AAG 2924
Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Gly Lys 742

AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966
Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu Phe Ser Thr Ser 756

GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013
Val Val His Thr Lys Stop                                761

TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063

AATTTTTAAG TATTTGAGTT TGAACAGATT AGCTCTGGGG GGAGGGGGTT 3113

TCCACAATGT GAGGGGGAAC CAAGAAAATT TTAAATACAG TGTATTTTCC 3163

AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG          3205
```

FIG. 11D

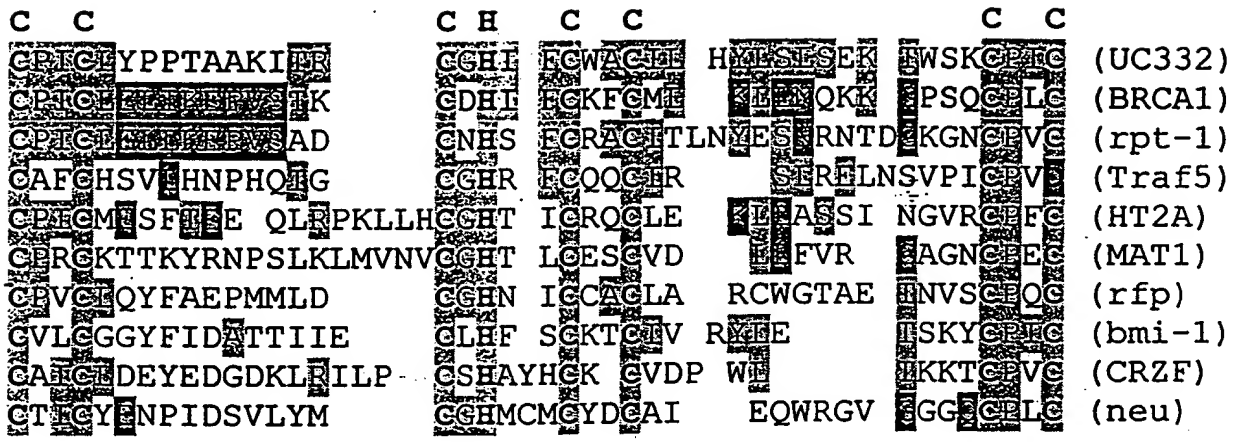

C C C H C C C C
CPICLYPPTAAKI TR CGHI FCWACLF HYLSLSEK TWSK CPLC (UC332)
CPICL TK CDHI FCKFCMT KEENQKK IPSQCPLC (BRCA1)
CPICL AD CNHS FCRACITLNYESNRNTDKKGNCPVC (rpt-1)
CAFGHSV HNPHQTG CGHR FCQQCIR STRELNSVPICPV (Traf5)
CPLCMLSFLFE QLRPKLLHCGHT ICRQCLE KLFASSI NGVRCPFC (HT2A)
CPRCKTTKYRNPSLKLMVNVCGHT LCESCVD FFVR AGNCPEC (MAT1)
CPVCLQYFAEPMMLD CGHN ICCACLA RCWGTAE TNVSCPQC (rfp)
CVLCGGYFIDATTIIE CLHF SCKTCIV RYFE TSKYCPLC (bmi-1)
CAICLDEYEDGDKLRILP CSHAYHCK CVDP WF IKKTCPVC (CRZF)
CTLCYENPIDSVLYM CGHMCMCYDCAI EQWRGV GGGCPLC (neu)

FIG. 12

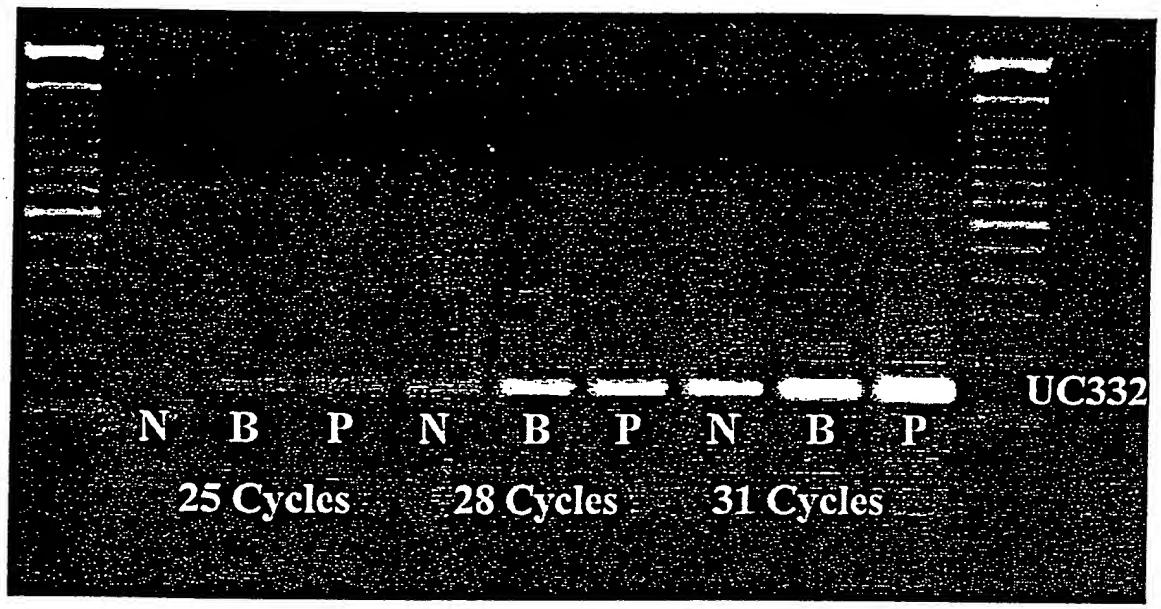


FIG. 13A

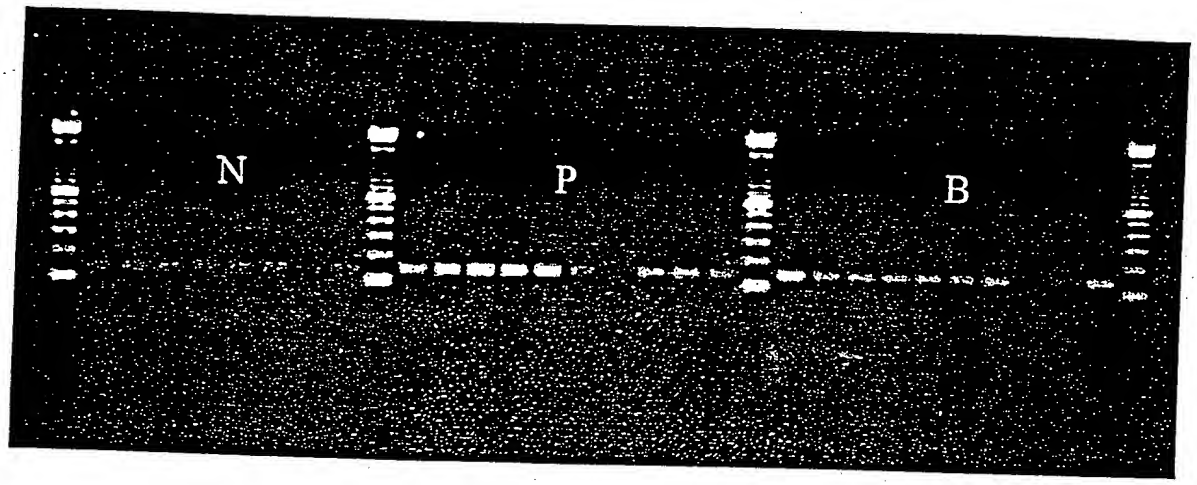


FIG. 13B

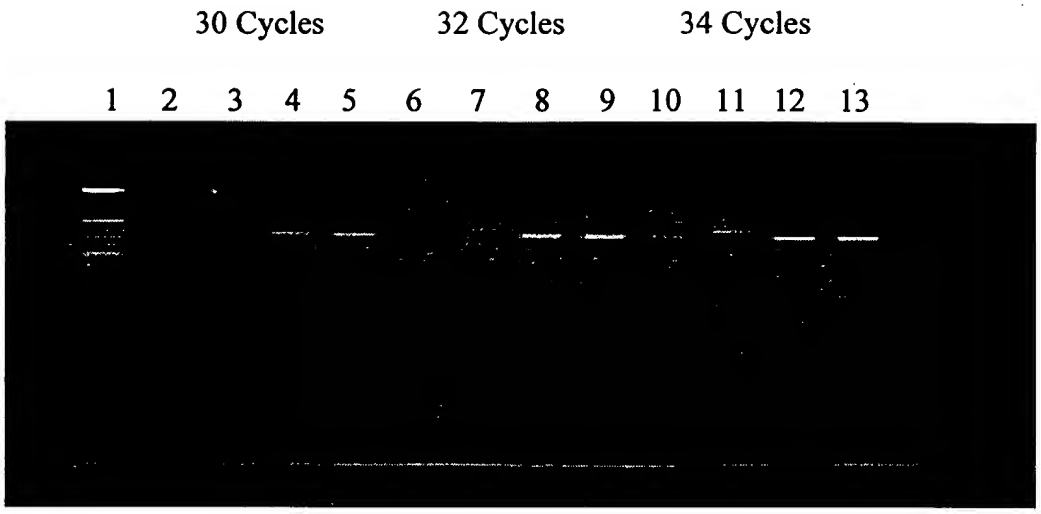


FIG. 14

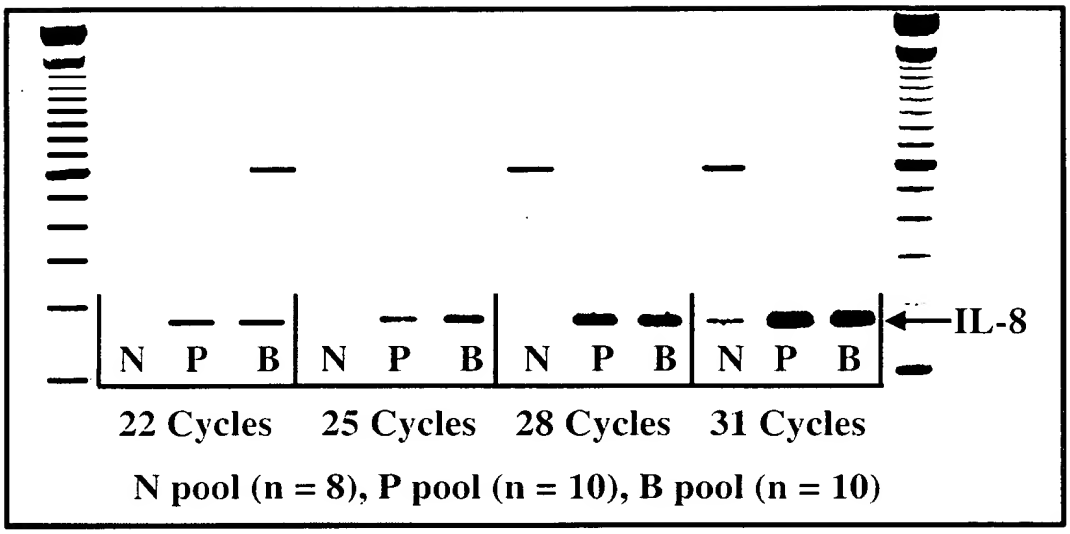

IL-8
N P B N P B N P B N P B
22 Cycles 25 Cycles 28 Cycles 31 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 1A

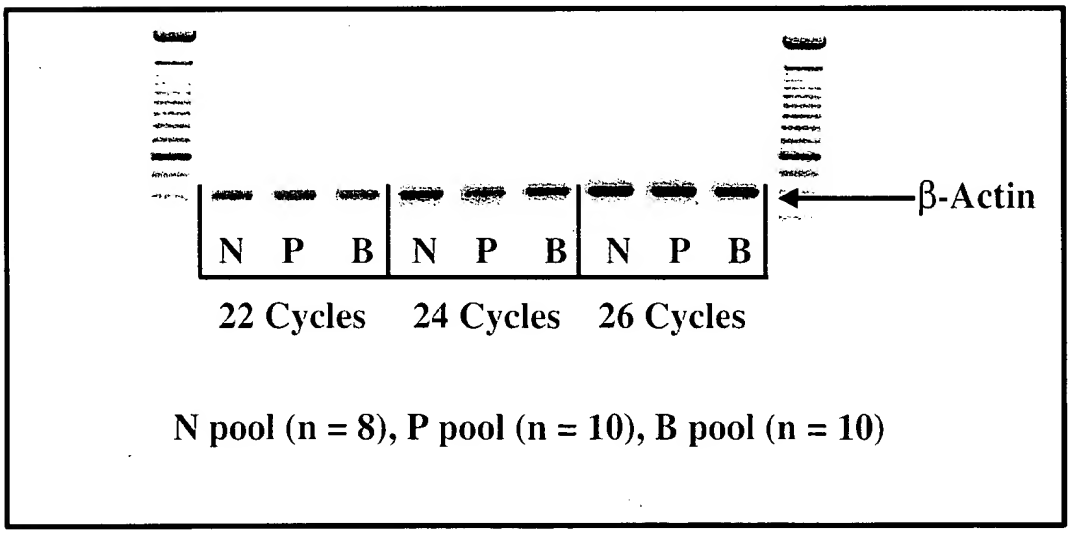

β-Actin
N P B N P B N P B
22 Cycles 24 Cycles 26 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 1B

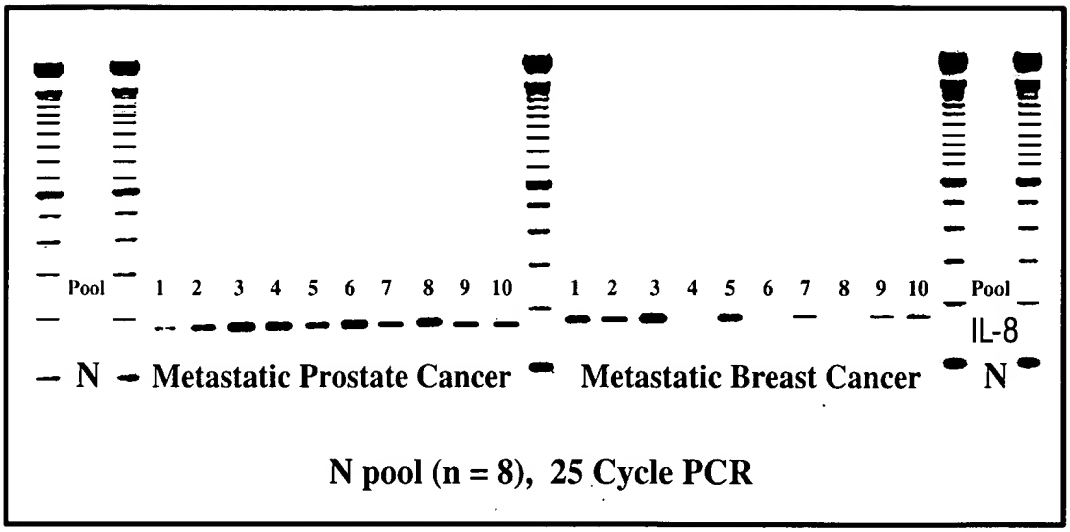

Pool
1 2 3 4 5 6 7 8 9 10
1 2 3 4 5 6 7 8 9 10
Pool
IL-8
N
Metastatic Prostate Cancer
Metastatic Breast Cancer
N
N pool (n = 8), 25 Cycle PCR

FIG. 2A

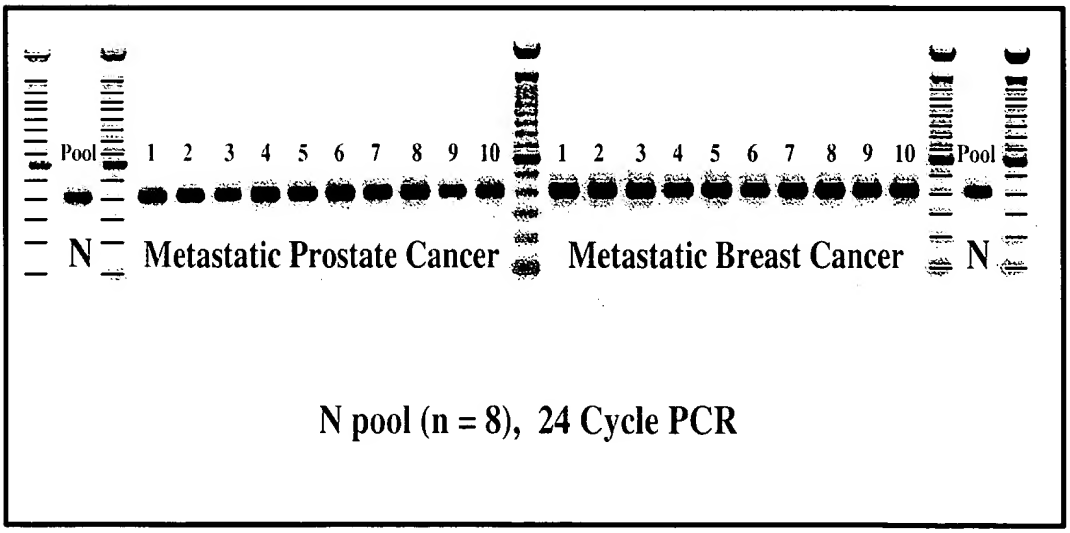

Pool
1 2 3 4 5 6 7 8 9 10
1 2 3 4 5 6 7 8 9 10
Pool
N
Metastatic Prostate Cancer
Metastatic Breast Cancer
N
N pool (n = 8), 24 Cycle PCR

FIG. 2B

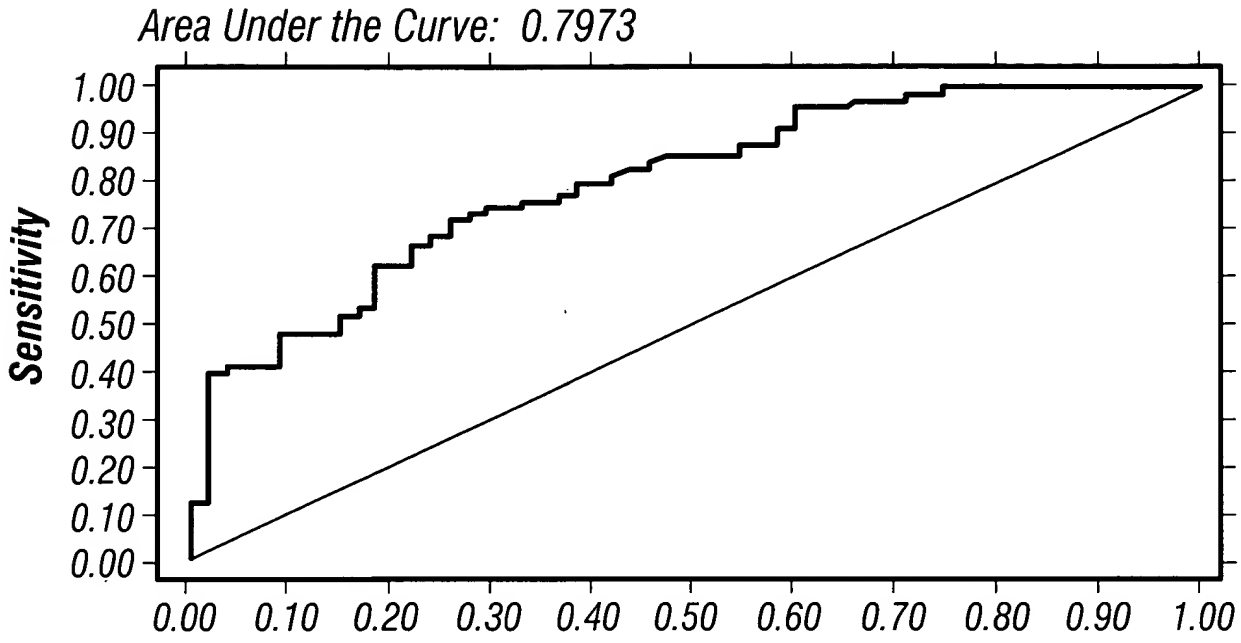

Area Under the Curve: 0.7973
Sensitivity
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0.00 0.10 0.20 0.30 0.40 0.50 0.60 0.70 0.80 0.90 1.00
1-Specifity

FIG. 3

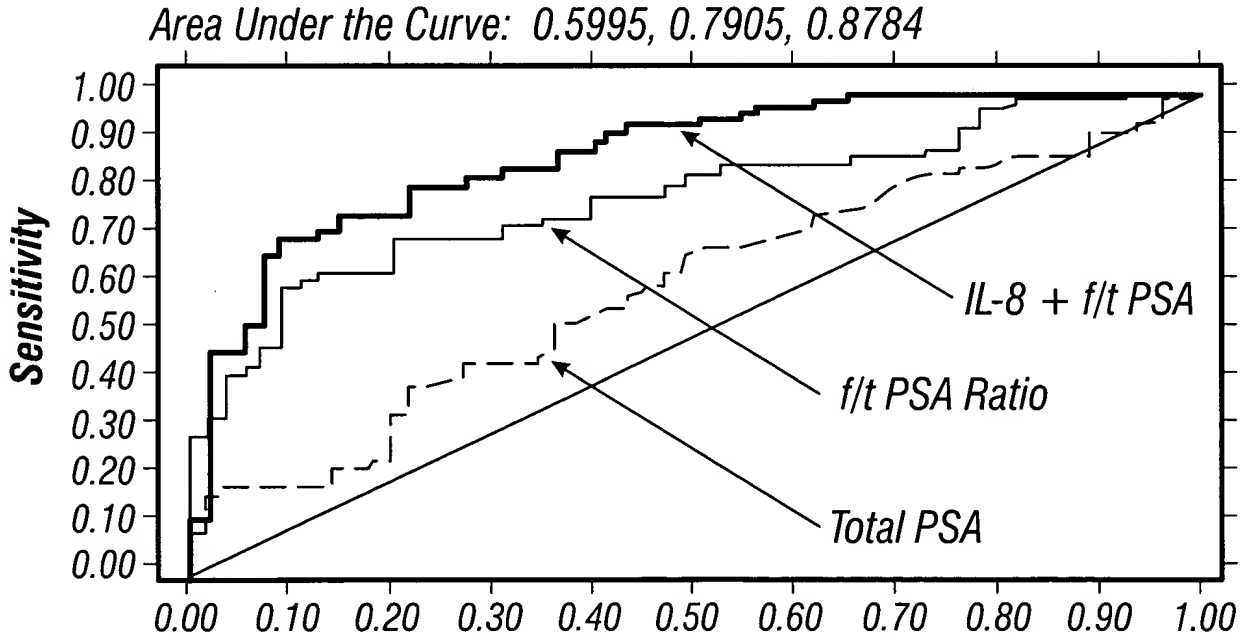

Area Under the Curve: 0.5995, 0.7905, 0.8784
Sensitivity
1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0.00 0.10 0.20 0.30 0.40 0.50 0.60 0.70 0.80 0.90 1.00
1-Specifity
IL-8 + f/t PSA
f/t PSA Ratio
Total PSA

FIG. 4

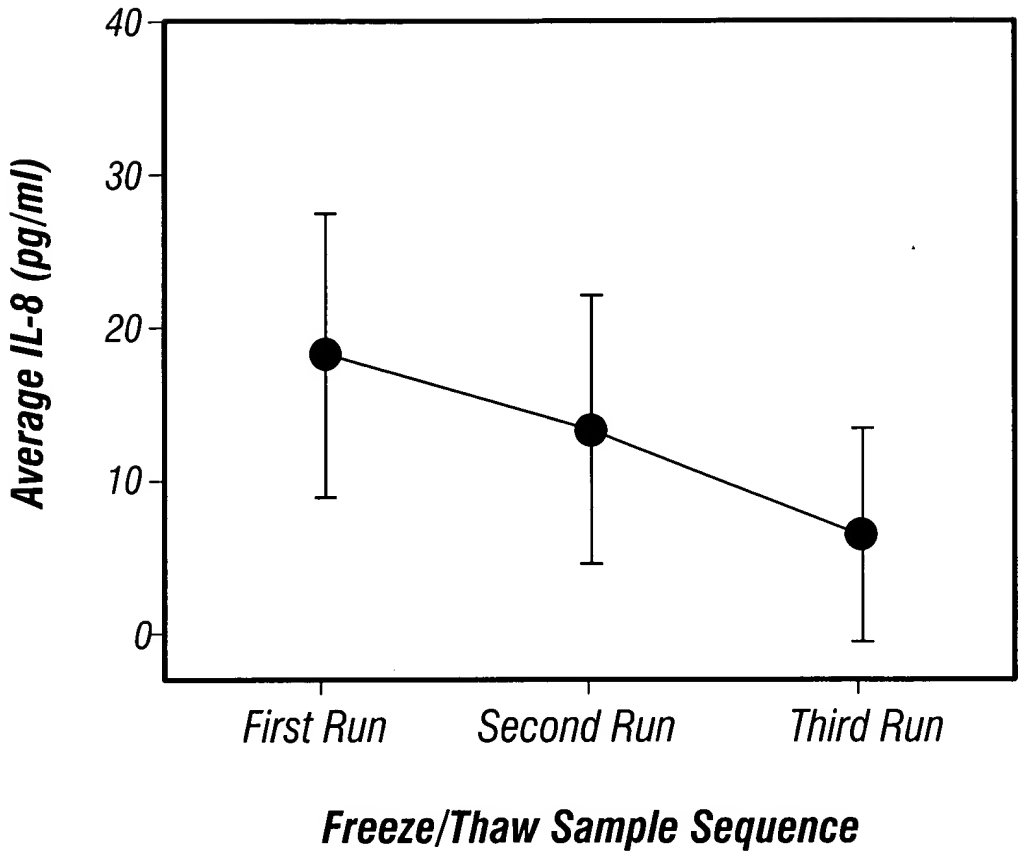

40
30
20
10
0
Average IL-8 (pg/ml)
First Run
Second Run
Third Run
Freeze/Thaw Sample Sequence

FIG. 5

```
                                  30                                  60
GCGGCAGGCGCGGCAAATTACGTTGCCGGAGCTGAACGGCGCGGCTGGTCTGAAGGCAAA HUM-UC331
                                  90                                 120
CAAGCGAGCGAGCGCGCGATAGGGGCCGAGAGGACGCGCAGGTGGCGGCGTTGCCATGTC HUM-UC331
                                                          START
                                 150                                 180
GCACGGTCACAGCCACGGCGGGGGTGGCTGCCGCTGCGCCGCCGAACGGGAGGAGCCGCC HUM-UC331
                                 210                                 240
CGAGCAGCGCGGCCTGGCCTACGGCCTGTACCTGCGCATCGACCTGGAGCGGCTGCAATG HUM-UC331
                                 270                                 300
CCTTAACGAGAGCCGCGAGGGCAGCGGCCGCGGCGTCTTCAAGCCATGGGAGGAGCGGAC HUM-UC331
                                                TTTCAAGCCGTGGGAGGA-CGGAC MOU-UC331
                                                *                   *
                                 330                                 360
CGACCGCTCCAAGTTTATTGAAAGTGATGCAGATGAAGAGCTTCTGTTTAATATTCCATT HUM-UC331
CGACCGCTCCAAGTTCGCTGAAAGTGATGCGGACGAAGAGCTCCTGTTTAATATTCCGTT MOU-UC331
                  * *               *  *         *                *
                                 390                                 420
TACGGGCAATGTCAAGCTCAAAGGCATCATTATAATGGGAGAGGATGATGACTCACACCC HUM-UC331
TACGTGCAATGTCAAGCTGAAAGGCGTCATCATAATGGGCGAGGATGATGACTCGCACCC MOU-UC331
    *               *       *    *         *                *
                                 450                                 480
CTCTGAGATGAGACTGTACAAGAATATTCCACAGATGTCCTTTGATGATACAGAAAGGGA HUM-UC331
CTCGGAGATGAGACTGTACAAGAACATTCCACAGATGTCATTTGATGACACAGAAAGGGA MOU-UC331
   *                        *                 *         *
```

FIG. 6A

```
                                510                                 540
GCCAGATCAGACCTTTAGTCTGAACCGGGATCTTACAGGAGAATTAGAGTATGCTACAAA HUM-UC331
GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAATTAGAATATGCTACGAA MOU-UC331
                  *            *  **                 *        *
                                570                                 600
AATTTCTCGTTTTTCAAATGTCTATCATCTCTCAATTCATATTTCAAAAAACTTCGGAGC HUM-UC331
AATCTCCAGGTTTTCAAATGTCTATCATCTTTCCATTCATATTTCAAAAAACTTTGGAGC MOU-UC331
   *   *   *                    ** *   *                    *
                                630                                 660
AGATACGACAAAGGTCTTTTATATTGGCCTGAGAGGAGAGTGGACTGAGCTTCGCCGACA HUM-UC331
AGATACGACGAAGATCTTTTATATTGGCCTGCGGGGAGAGTGGACTGAGCTTCGCCGGCA MOU-UC331
          *    *                    * *                        *
                                690                                 720
CGAGGTGACCATCTGCAATTACGAAGCATCTGCCAACCCAGCAGACCATAGGGTCCATCA HUM-UC331
TGAGGTGACCATCTGCAACTATGAAGCGTCAGCCAACCCAGCAGACCACCGGGTGCATCA MOU-UC331
*                   *   *      *   *                    **     *
                                750                                 780
GGTTACCCCACAGACACACTTTATTTCCTAAGGGCTGGCCAAGGCTCCCATAGAGGCGCT HUM-UC331
GGTCACCCCGCAGACACACTTCATTTCTTAAGGGCCAGCCGGGGCTCCCTCAGATGCGCT MOU-UC331
   *      *              *      *STOP    **    **         **    *
                                810                                 840
GTGTCAGTGAAGATGTACGACTACCTGTTGGGAAGGACAAAGGGATGAGGCTCCAGAGAG HUM-UC331
GTTAGTGAA--GATGTGCGACCACCTGCTGGGAAGGACAGAGG-ATG---CTCCAGCAAT MOU-UC331
  **** ****      *     *      *              *    *    ***       ** *
```

FIG. 6B

```
                                870                                 900
AGTTGGCTGCCACAGCTCTG-CCAAGCTTTGTCTTTGGGGCTTGCTGCAGAAACCTGGCC HUM-UC331
AGTTGCCTGCCAGAGCTTTGGCCAGGCTTTGTC-TCGGGG-TTGCTGCAGGAACCTGGCC MOU-UC331
     *       *    *  *    *        * *    *          *

                                930                                 960
TACGGAAGATACGACACCACTGGGAGGGTTGTGTAGGTGCCAGGGGACCATCGTGGTTCT HUM-UC331
TGTGGAAACCGCCTCACCACCAGGAGCG--GTATGGGTGCCAAGGGA---TAGTCTCTCT MOU-UC331
 **    **** **       **    * **  * *        *    *** *  ***

                                990                                1020
CTAGGGCGCTGTGGAAATTGGGTCTTGGGCTGGGTGGCATCTGGCAGTCATGGGTAACAC HUM-UC331
CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAGTCATGAATAATGC MOU-UC331
   *   *   **    *         *                   *         **   **

                               1050                                1080
TTGCTTTTCCAGTTAATGTGGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT HUM-UC331
TCACTT-CCCAGTC--TGTGGCCACGGGATCCCATGTGTCTTTTTGCTT-GATTTCTTGT MOU-UC331
 **   **      ***         * *   *   *     * *      *  *******

                               1110                                1140
GTTGTGTGACTTGTTTTTTTGATTTTGTATTTGTTTTTTTAAAGGAAACTATTTGTGGGC HUM-UC331
GTGGTTTGTCCT-TTTGTGGCA-------------TCAAAAAGGATGCTTCCTTGACCG MOU-UC331
  *   *   *    *   * *** ************** ***      **  *** ******

                               1170                                1200
TATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTAGCCATCAGGAGGGTCTCC HUM-UC331
TAGAAT---CCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGGTCTCC MOU-UC331
  * ***** *       **  **** *  *     *  **
```

FIG. 6C

```
                                1230                                1260
AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTCCCCTCTCATTGTTCAGCATTCTTGTC HUM-UC331
AGCTAGAAACACTTCGTCCCTGCTTGCTCCT-CCTCCTGTCATTGCTCAGCATTCGTGTC MOU-UC331
 *   *         *  *               ** *   *       *          *

                                1290                                1320
AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGG HUM-UC331
AGGGTGCCTAGCT-GGTGTCACATATCAGACACAAGTGTCCCACAATGGTGGTTGGAAAG MOU-UC331
 * *    *    *  *  **** *   **    *       ***** ** * * *   *

                                1350                                1380
ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGC HUM-UC331
GAAGGAGTCTCCTG---ATACATGACTGCTT------GGGG--AAGG-CTTACACAGT-C MOU-UC331
**              ***  * *   **    ******    **    *   ***  * *

                                1410                                1440
CTAGCTAAGCAGTCTGGGGAGAGCATGGGGATCATTTCTATGTGTGTGGGTAATCTGGTC HUM-UC331
TAGCCAAATTAGTT--GCGAG----------TCCTTTCCCTGTGT--GGGTGACCTGGTT MOU-UC331
**** *  **   *** *   **********  *    **     **    * *     *

                                1470                                1500
AG--TAAGATTGAGACTTAGTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT HUM-UC331
GGGGTAAAACTGAGACAG--TAAAGATTCCTCTTGGGACCTCCTTGGTGTTTCCCTGCTT MOU-UC331
* **   * *       **** *         *     * **     **     ****

                                1530                                1560
CTAACTAGTGTTGTAAGTCCGATGCCAGAATTTGGAGATTTGAGTTCTTCTTTTCATGGC HUM-UC331
CTAACTCATGTTATAAACCCAGGGCTGGAGTCTGGAGACCCTGCTCCTTCTGTTCATGGC MOU-UC331
      **    *   **  ***  **  * *      ****** *     *
```

FIG. 6D

```
                                1590                                1620
TTTTATTCACTGTGACTAATAAGCTTCCTAATAAATCCTTGCCAGACTTAAAAAAAAAAA HUM-UC331
TTTCATTCATGGTGACTAATGAGCTTCCTAATAAATCCTTAG-AGACTTAAAA        MOU-UC331
   *     **          *                      * *
```

FIG. 6E

```
         10         20         30         40
 MSHGHSHGGGGCRCAAER-EEPPEQRGLAYGLYLRIDLE HUM-UC331
>CSHGHSHN-----CAAEHIPEVPGDDVYRYDMVSYIDME ZK353.1

         50         60         70         80
RLQCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF HUM-UC331
                 >FKPWEERTDRSKFAESDADEELLF MOU-UC331
KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF ZK353.1

         90        100        110        120
NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPQMSFDD HUM-UC331
NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPQMSFDD MOU-UC331
NIPFTGHVRLTGLSIIGDEDGSHPAKIRLFKDREAMSFDD ZK353.1

        130        140        150        160
TEREPDQTFSLNRDLTGELEYATKISRFSNVYHLSIHISK HUM-UC331
TEREPEQTFSLNRDITGELEYATKISRFSNVYHLSIHISK MOU-UC331
CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA ZK353.1

        170        180        190        200
NFGADTTKVFYIGLRGEWTELRRHEVTICNYEASANPADH HUM-UC331
NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH MOU-UC331
NFGEDETKIYYIGLRGEFQHEFRQRIAIATYESRAQLKDH ZK353.1

        210
RVHQVTPQTHFIS. HUM-UC331
RVHQVTPQTHFIS. MOU-UC331
KNEIPDAVAKGLF. ZK353.1
```

FIG. 7

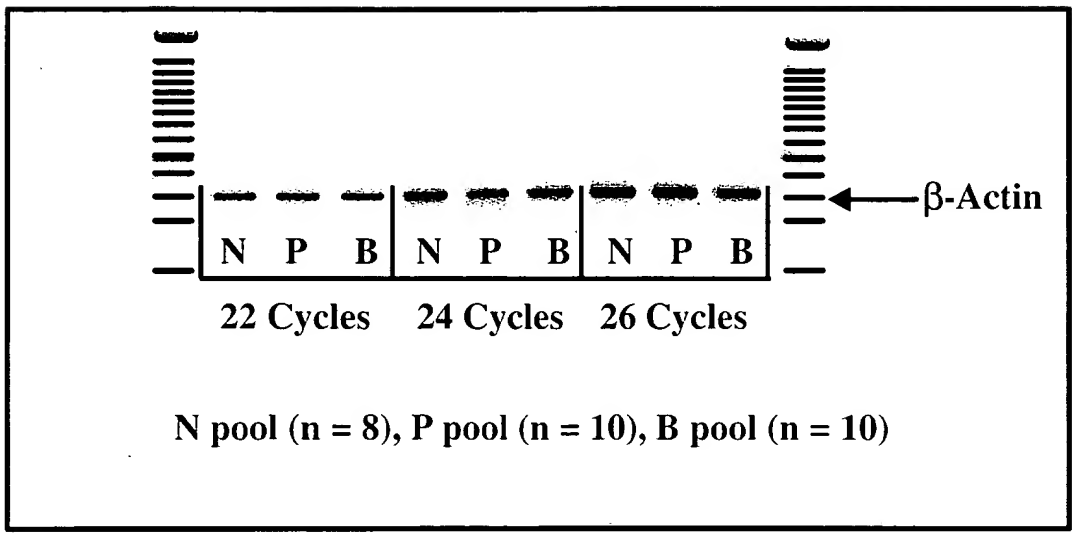

β-Actin
N P B N P B N P B
22 Cycles 24 Cycles 26 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 8A

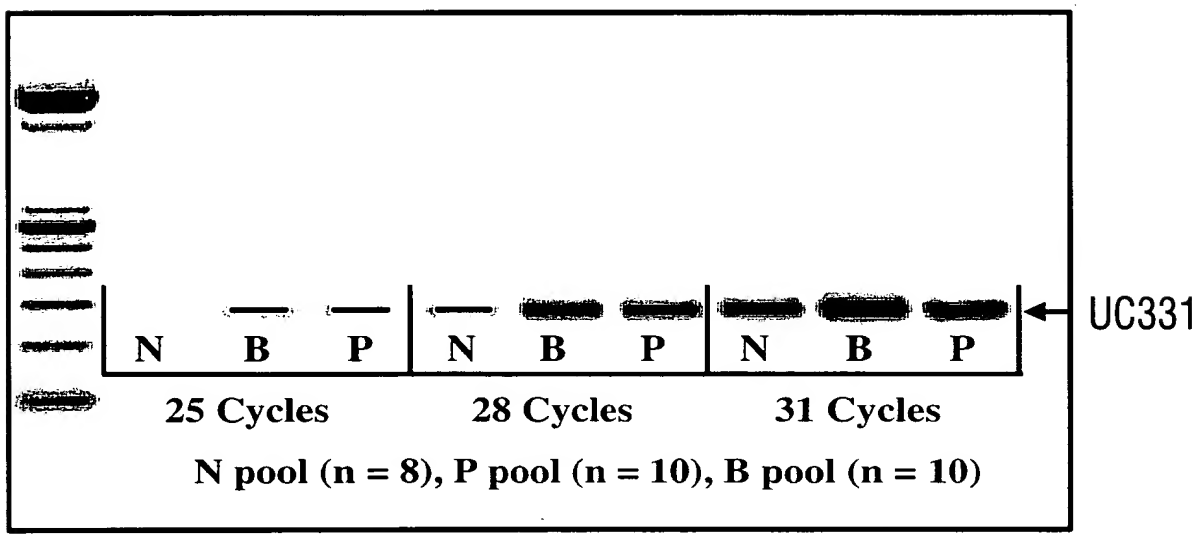

UC331
N B P N B P N B P
25 Cycles 28 Cycles 31 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 8B

DATED: 8/30/96

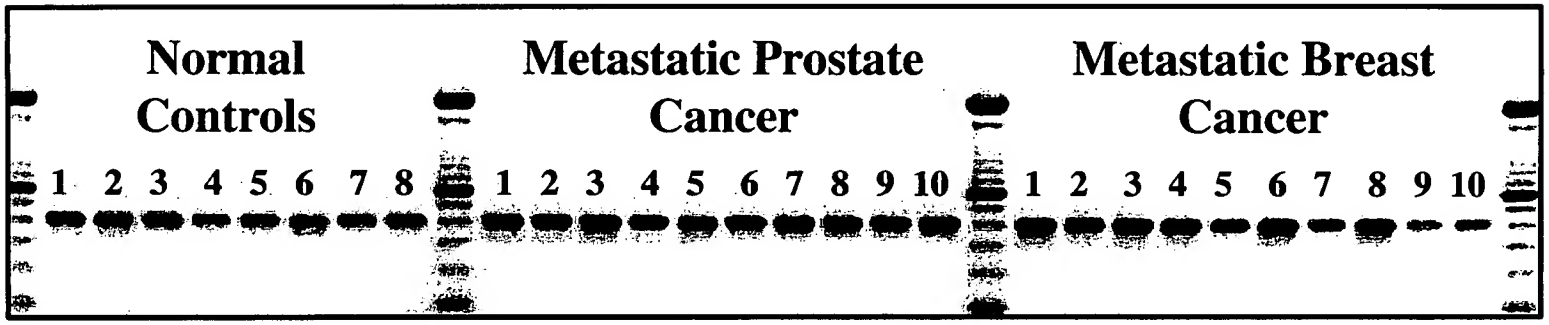


FIG. 9A

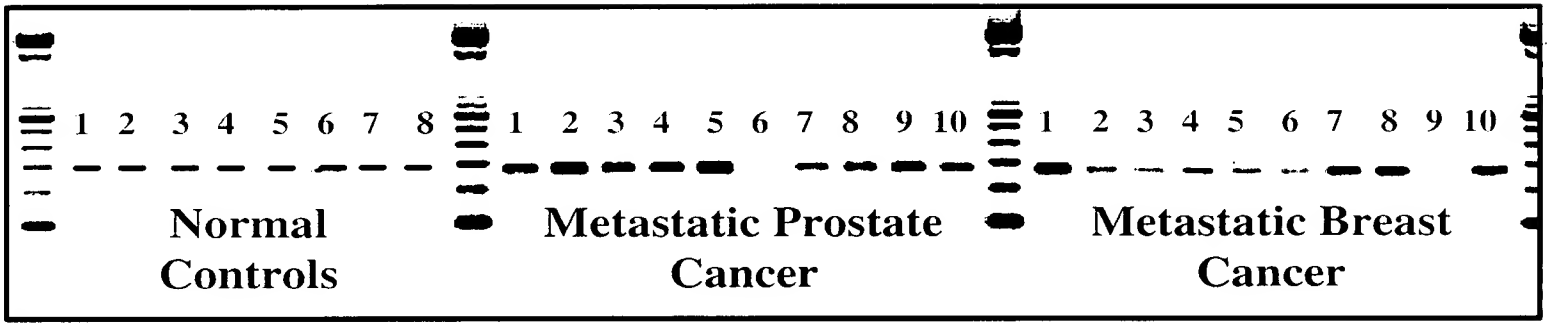


FIG. 9B

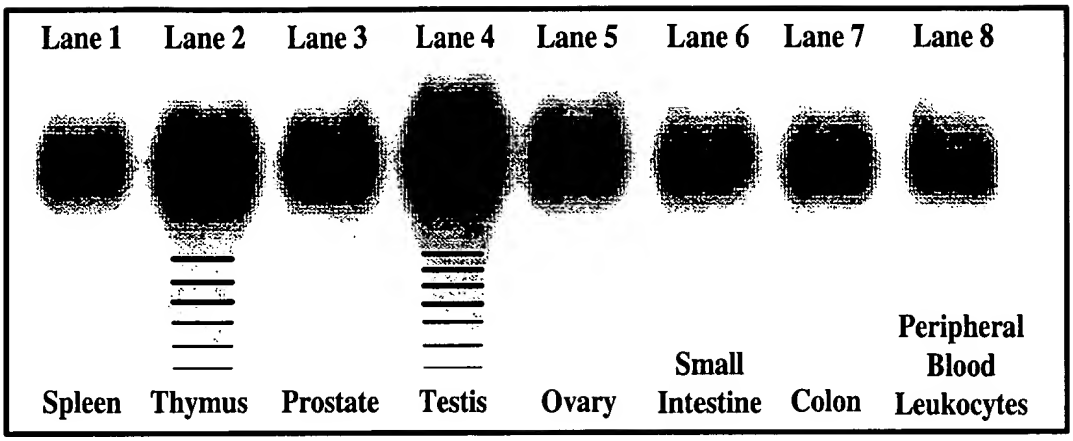

Lane 1
Lane 2
Lane 3
Lane 4
Lane 5
Lane 6
Lane 7
Lane 8
Spleen
Thymus
Prostate
Testis
Ovary
Small Intestine
Colon
Peripheral Blood Leukocytes

FIG. 10

```
        10          20          30          40          50
CGACTCGTCG CCATTCCCGG AGCAGGTCGG CCTCGGCCCA GGGGCGAGTA
        60          70          80          90         100
TCCGTTGCTG TGTCGGAGAC ACTAGTCCCC GACACCGAGA CAGCCAGCCC
       110         120         130         140         150
TCTCCCCTGC CTCGCGGCGG GAGAGCGTGT CCGGCCGGCC GGCCGGCGGG
       160         170         180         190         200
GCTCGCGCAA CCTCCCTCGC CTCCCCTTCC CCCGCAGCCT CCGCCCCGCC
       210         220         230         240         250
AGGCCCGGCC CGGACTCCCG AGCCCCGGCC TCCTCGTCCT CGGTCGCCGC
       260         270         280         290         300
TGCCGCCGGG CTTAACAGCC CCGTCCGCCG CTTCTCTTCC TAGTTTGAGA
       310         320         330         340         350
AGCCAAGGAA GGAAACAGGG AAAAATGTCG CCATGAAGGC CGAGAACCGC
       360         370         380         390         400
TGCCGCCGCC GACCCCCGCC GGCCCTGAAC GCCATGAGCC TGGGTCCCCG
       410         420         430         440         450
CCGCGCCCGC TCCGCTCCGA CTGCCGTCGC CGCCGAGGCC CCCGTTGATG
       460         470         480         490         500
CCGCTGAGCT CCCCCAACGC CGCCGCCACC GCCTCCGACA TGGACAAGAA
       510         520         530         540         550
CAGCGGCTCC AACAGCTCCT CCGCCTCTTC GGGCAGCAGC AAAGGGCAAC
       560         570         580         590         600
AGCCGCCCCG CTCCGCCTCG GCGGGGCCAG CCGGCGAGTC TAAACCCAAG
```

FIG. 11A

```
       610         620         630         640         650
AGCGAATTAC TAATTTCAGC TGGATTCAAT TTGTTGTCAG TTGATTCTGT
       660         670         680         690       698
AGTAAGGCCA TATGTTGCCC CTCTGGAGGT GCTTGTCAAC TACTCTGG

ATG ATG GAT GGA AAG AAC TCC AGT GGA TCC AAG CGT TAT AAT 740
Met Met Asp Gly Lys Asn Ser Ser Gly Ser Lys Arg Tyr Asn 14

CGC AAA CGT GAA CTT TCC TAC CCC AAA AAT GAA AGT TTT AAC 782
Arg Lys Arg Glu Leu Ser Tyr Pro Lys Asn Glu Ser Phe Asn 28

AAC CAG TCC CGT CGC TCC AGT TCA CAG AAA AGC AAG ACT TTT 824
Asn Gln Ser Arg Arg Ser Ser Ser Gln Lys Ser Lys Thr Phe 42

AAC AAG ATG CCT CCT CAA AGG GGC GGC GGC AGC AGC AAA CTC 866
Asn Lys Met Pro Pro Gln Arg Gly Gly Gly Ser Ser Lys Leu 56

TTT AGC TCT TCT TTT AAT GGT GGA AGA CGA GAT GAG GTA GCA 908
Phe Ser Ser Ser Phe Asn Gly Gly Arg Arg Asp Glu Val Ala 70

GAG GCT CAA CGG GCA GAG TTT AGC CCT GCC CAG TTC TCT GGT 950
Glu Ala Gln Arg Ala Glu Phe Ser Pro Ala Gln Phe Ser Gly 84

CCT AAG AAG ATC AAC CTG AAC CAC TTG TTG AAT TTC ACT TTT 992
Pro Lys Lys Ile Asn Leu Asn His Leu Leu Asn Phe Thr Phe 98
```

FIG. 11B

```
GAA CCC CGT GGC CAG ACG GGT CAC TTT GAA GGC AGT GGA CAT 1034
Glu Pro Arg Gly Gln Thr Gly His Phe Glu Gly Ser Gly His 112

GGT AGC TGG GGA AAG AGG AAC AAG TGG GGA CAT AAG CCT TTT 1076
Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe 126

AAC AAG GAA CTC TTT TTA CAG GCC AAC TGC CAA TTT GTG GTG 1118
Asn Lys Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val 140

TCT GAA GAC CAA GAC TAC ACA GCT CAT TTT GCT GAT CCT GAT 1160
Ser Glu Asp Gln Asp Tyr Thr Ala His Phe Ala Asp Pro Asp 154

ACA TTA GTT AAC TGG GAC TTT GTG GAA CAA GTG CGC ATT TGT 1202
Thr Leu Val Asn Trp Asp Phe Val Glu Gln Val Arg Ile Cys 168

AGC CAT GAA GTG CCA TCT TGC CCA ATA TGC CTC TAT CCA CCT 1244
Ser His Glu Val Pro Ser Sys Pro Ile Cys Leu Tyr Pro Pro 182

ACT GCA GCC AAG ATA ACC CGT TGT GGA CAC ATC TTC TGC TGG 1286
Thr Ala Ala Lys Ile Thr Arg Cys Gly His Ile Phe Cys Trp 196

GCA TGC ATC CTG CAC TAT CTT TCA CTG AGT GAG AAG ACG TGG 1328
Ala Cys Ile Leu His Tyr Leu Ser Leu Ser Glu Lys Thr Trp 210
```

FIG. 11C

```
AGT AAA TGT CCC ATC TGT TAC AGT TCT GTG CAT AAG AAG GAT 1370
Ser Lys Cys Pro Ile Cys Tyr Ser Ser Val His Lys Lys Asp 224

CTC AAG AGT GTT GTT GCC ACA GAG TCA CAT CAG TAT GTT GTT 1412
Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val 238

GGT GAT ACC ATT ACG ATG CAG CTG ATG AAG AGG GAG AAA GGG 1454
Gly Asp Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly 252

GTG TTG GTG GCT TTG CCC AAA TCC AAA TGG ATG AAT GTA GAC 1496
Val Leu Val Ala Leu Pro Lys Ser Lys Trp Met Asn Val Asp 266

CAT CCC ATT CAT CTA GGA GAT GAA CAG CAC AGC CAG TAC TCC 1538
His Pro Ile His Leu Gly Asp Glu Gln His Ser Gln Tyr Ser 280

AAG TTG CTG CTG GCC TCT AAG GAG CAG GTG CTG CAC CGG GTA 1580
Lys Leu Leu Leu Ala Ser Lys Glu Gln Val Leu His Arg Val 294

GTT CTG GAG GAG AAA GTA GCA CTA GAG CAG CAG CTG GCA GAG 1622
Val Leu Glu Glu Lys Val Ala Leu Glu Gln Gln Leu Ala Glu 308

GAG AAG CAC ACT CCC GAG TCC TGC TTT ATT GAG GCA GCT ATC 1664
Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala Ala Ile 322
```

FIG. 11D

```
CAG GAG CTC AAG ACT CGG GAA GAG GCT CTG TCG GGA TTG GCC 1706
Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala 336

GGA AGC AGA AGG GAG GTC ACT GGT GTT GTG GCT GCT CTG GAA 1748
Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu 350

CAA CTG GTG CTG ATG GCT CCC TTG GCG AAG GAG TCT GTT TTT 1790
Gln Leu Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe 364

CAA CCC AGG AAG GGT GTG CTG GAG TAT CTG TCT GCC TTC GAT 1832
Gln Pro Arg Lys Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp 378

GAA GAA ACC ACG GAA GTT TGT TCT CTG GAC ACT CCT TCT AGA 1874
Glu Glu Thr Thr Glu Val Cys Ser Leu Asp Thr Pro Ser Arg 392

CCT CTT GCT CTC CCT CTG GTA GAA GAG GAG GAA GCA GTG TCT 1916
Pro Leu Ala Leu Pro Leu Val Glu Glu Glu Glu Ala Val Ser 406

GAA CCA GAG CCT GAG GGG TTG CCA GAG GCC TGT GAT GAC TTG 1958
Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala Cys Asp Asp Leu 420

GAG TTA GCA GAT GAC AAT CTT AAA GAG GGG ACC ATT TGC ACT 2000
Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile Cys Thr 434
```

FIG. 11E

```
GAG TCC AGC CAG CAG GAA CCC ATC ACC AAG TCA GGC TTC ACA 2042
Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr 448

CGC CTC AGC AGC TCT CCT TGT TAC TAC TTT TAC CAA GCG GAA 2084
Arg Leu Ser Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu 462

GAT GGA CAG CAT ATG TTC CTG CAC CCT GTG AAT GTG CGC TGC 2126
Asp Gly Gln His Met Phe Leu His Pro Val Asn Val Arg Cys 476

CTC GTG CGG GAG TAC GGC AGC CTG GAG AGG AGC CCC GAG AAG 2168
Leu Val Arg Glu Tyr Gly Ser Leu Glu Arg Ser Pro Glu Lys 490

ATC TCA GCA ACT GTG GTG GAG ATT GCT GGC TAC TCC ATG TCT 2210
Ile Ser Ala Thr Val Val Glu Ile Ala Gly Tyr Ser Met Ser 504

GAG GAT GTT CGA CAG CGT CAC AGA TAT CTC TCT CAC TTG CCA 2252
Glu Asp Val Arg Gln Arg His Arg Tyr Leu Ser His Leu Pro 518

CTC ACC TGT GAG TTC AGC ATC TGT GAA CTG GCT TTG CAA CCT 2294
Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu Ala Leu Gln Pro 532

CCT GTG GTC TCT AAG GAA ACC CTA GAG ATG TTC TCA GAT GAC 2336
Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser Asp Asp 546
```

FIG. 11F

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ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378
Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560

GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420
Glu Arg Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574

AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462
Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

CTA CAG CAG TTT CCT GCC TTC AAT TCT TAT ACC TGC TCC TCT 2504
Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602

GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546
Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616

CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588
Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630

GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630
Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644

AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672
Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658
```

FIG. 11G

```
TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714
Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672

GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756
Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686

AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798
Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700

GAT AAT TCA GAC CGT GTT CCT GTG CCC AGT TTT CAA AAT TCC 2840
Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714

TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882
Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728

CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA GGA AAG 2924
Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Gly Lys 742

AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966
Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu Phe Ser Thr Ser 756

GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013
Val Val His Thr Lys Stop                               761
```

FIG. 11H

```
TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063

AATTTTTAAG TATTTGAGTT TGAACACATT AGCTCTGGGG GGAGGGGGTT 3113

TCCACAATGT GAGGGGGAAC CAAGAAAATT TTAAATACAG TGTATTTTCC 3163

AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG         3205
```

FIG. 11I

DATED: 8/5/03/96D

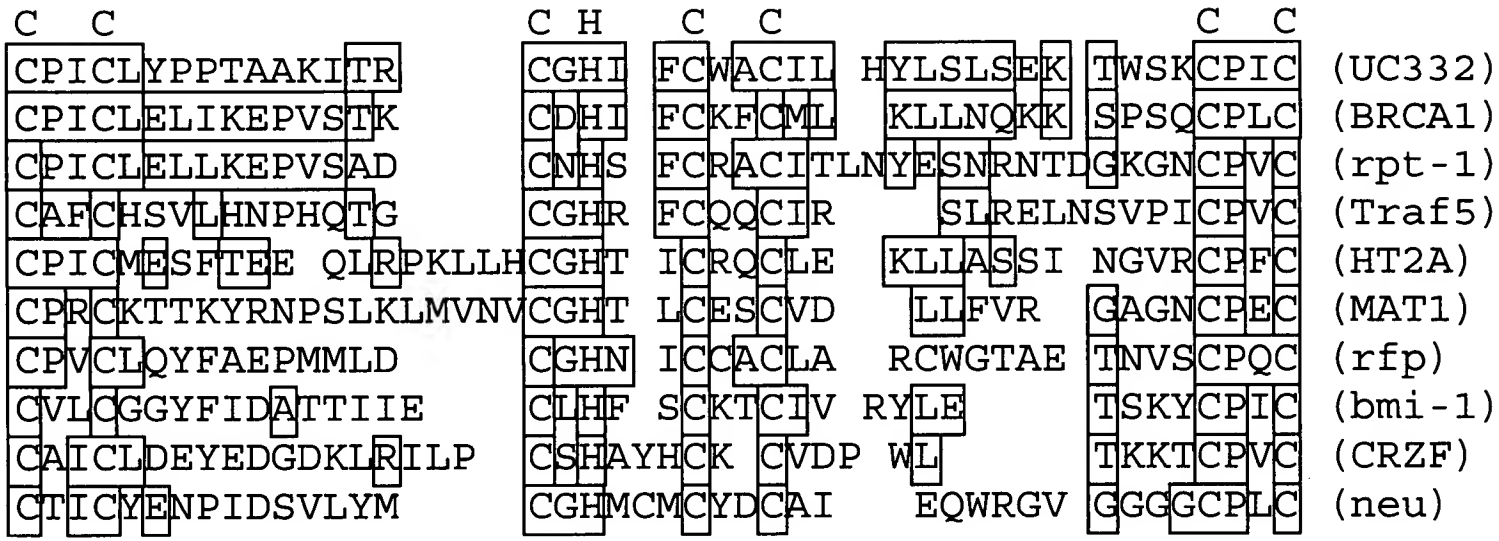

FIG. 12

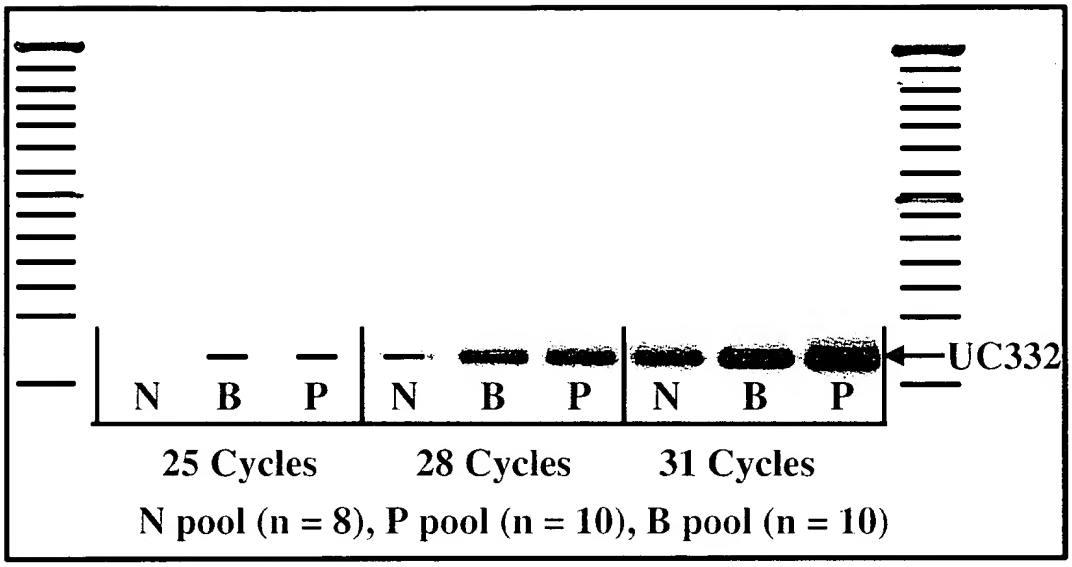
N B P N B P N B P
UC332
25 Cycles
28 Cycles
31 Cycles
N pool (n = 8), P pool (n = 10), B pool (n = 10)

FIG. 13A

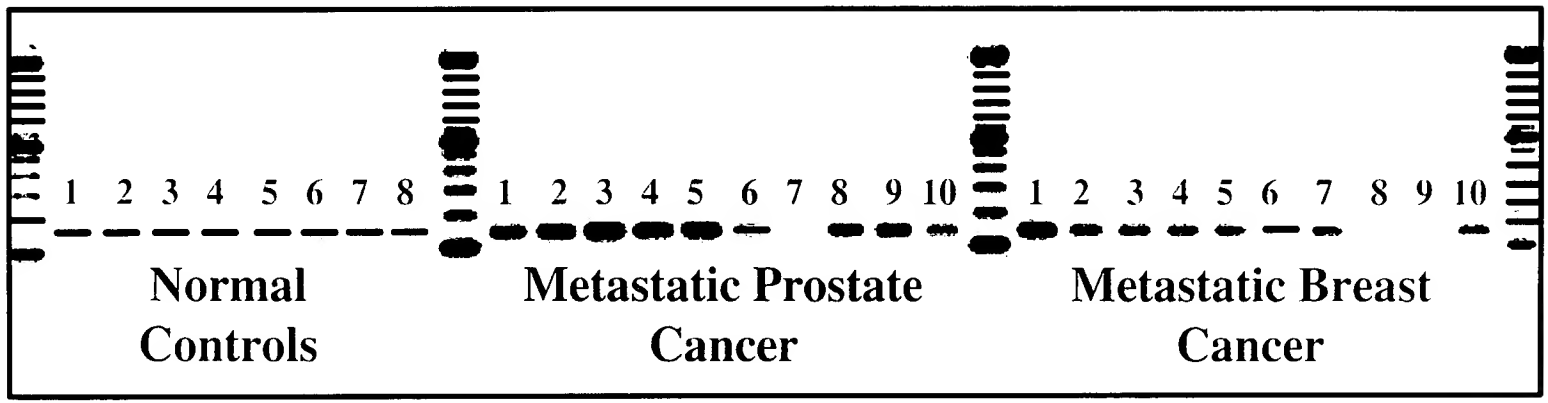

FIG. 13B

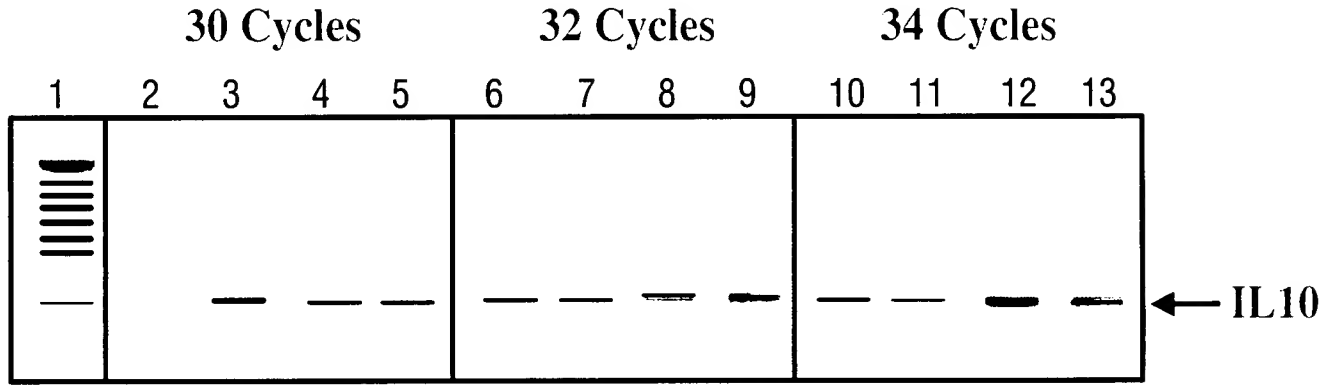

FIG. 14